Citation Evidence Report

EB-1B Petition — Outstanding Professor or Researcher

8 CFR § 204.5(i)(3) · Authorship + Original Contributions

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SCIEX

[Google Scholar profile]

Generated 2026-05-25 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

528	556	24	10
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.

90.4% independent of 512 classified citing papers

Citation type	Count
Independent	463
Self-citation	5
Co-author	44
Same-institution	0

16 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 advanced hydrogen exchange mass spectrometry methodologies to elucidate protease activation mechanisms and characterize protein-ligand interaction dynamics.

The researcher established a foundational contribution in structural biology through the 2013 paper on ClpP protease activation by ADEP antibiotics, utilizing hydrogen exchange mass spectrometry. This core work serves as the anchor for a subsequent line of inquiry into macromolecular dynamics.

This line of work appears to address the need for refined analytical techniques to study biological macromolecules. The 2014 follow-up papers suggest an expansion from specific case studies to broader methodological frameworks, examining both general mass spectrometry methods and the nuanced kinetics of protein-ligand interactions, including noncanonical scenarios.

The significance of this research is evidenced by substantial independent uptake. The core paper has garnered 62 citations, while the methodological follow-ups have accumulated 185 and 70 citations respectively. With 90.4% of citing papers originating from independent researchers, the work demonstrates broad relevance and adoption across the scientific community.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 288 **· 2 flagged influential by Semantic Scholar**

CORE PAPER

Activation of ClpP protease by ADEP antibiotics: insights from hydrogen exchange mass spectrometry

2013 · 62 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Mapping ligand binding using microfluidics-enabled millisecond timescale hydrogen-deuterium exchange	University of Toronto, York University	Canada	—
2	Integrative Structural Model of DNA-PKcs in the Initial Steps of Non-Homologous End Joining	University of Calgary	Canada	—
3	Characterizing Protein Dynamics of Protein-Ligand Interactions by Hydrogen-Deuterium Exchange Mass Spectrometry	University of Copenhagen, University of Southern Denmark, University of Vienna	Austria, Denmark	—
4	Advances in hydrogen/deuterium exchange mass spectrometry and the pursuit of challenging biological systems	Northeastern University	United States	—
5	Applications of hydrogen/deuterium exchange MS from 2012 to 2014	Northeastern University	United States	—
6	Localizing Carbohydrate Binding Sites in Proteins Using Hydrogen/Deuterium Exchange Mass Spectrometry	—	—	—
7	Allosteric regulation of human tryptophan hydroxylase isoform 2 (hTPH2)	Chemistry	—	—
8	Recent structural insights into the mechanism of ClpP protease regulation by AAA+ chaperones and small molecules	University of Toronto	Canada	—
9	Structural Insights into Bortezomib-Induced Activation of the Caseinolytic Chaperone-Protease System in Mycobacterium tuberculosis	—	—	—

No.	Citing paper	Citing institution(s)	Country	S2
10	The role of ClpP protease in bacterial pathogenesis and human diseases	—	—	—
11	AAA+ chaperones and acyldepsipeptides activate the ClpP protease via conformational control	—	—	—
12	Role and regulation of Clp proteases: A target against gram-positive bacteria	Universidad Andrés Bello	Chile	—
13	Conformational control of the bacterial Clp protease by natural product antibiotics	Compact Imaging (United States)	United States	—
14	Reprogramming of the caseinolytic protease by ADEP antibiotics: molecular mechanism, cellular consequences, therapeutic potential	—	—	—
15	EGCG has dual and opposing effects on the N-terminal region of self-associating α-synuclein oligomers	Aarhus University, Aarhus University | University of Southern Denmark, University of Southern Denmark	Denmark	—
16	Functional characterisation of ClpP mutations conferring resistance to acyldepsipeptide antibiotics in Firmicutes	—	—	—
17	Characterization of gain-of-function mutant provides new insights into ClpP structure	—	—	—
18	Acyldepsipeptide analogues: a future generation antibiotics for tuberculosis treatment	Durban University of Technology, University of the Western Cape, University of the Witwatersrand	South Africa	—
19	An amino acid domino effect orchestrates ClpP's conformational states	Center for Integrated Protein Science Munich	Germany	—
20	Piperine, an alkaloid inhibiting the super-relaxed state of myosin, binds to the myosin regulatory light chain	University of California, San Francisco, Washington State University	United States	—
21	Targeting mitochondrial proteases for therapy of acute myeloid leukaemia	West China Hospital, Sichuan University	China	—
22	Towards integrative structural mass spectrometry: Benefits from hybrid approaches	Université de Strasbourg	France	—
23	Acyldepsipeptide Antibiotics as a Potential Therapeutic Agent Against Clostridium Difficile Recurrent Infections	—	—	—
24	Acyldepsipeptide activated ClpP1P2 macromolecule of Leptospira, an ideal Achilles' heel to hamper the cell survival and deregulate ClpP proteolytic activity	Indian Institute of Technology Guwahati	India	—
25	The structure of caseinolytic protease subunit ClpP2 reveals a functional model of the caseinolytic protease system from Chlamydia trachomatis	Southern Illinois University Carbondale, University of Kansas Medical Center, University of Nebraska Medical Center	United States	—
26	Open and compressed conformations of Francisella tularensis ClpP	—	—	—

No.	Citing paper	Citing institution(s)	Country	S2
27	The future of drug discovery: enabling technologies for enhancing lead characterization and profiling therapeutic potential	—	—	—
28	Killing the survivors	—	—	—
29	Identification of lead molecules for the development of antivirals targeting the Ebola virus matrix protein VP40	Philipps-Universität Marburg	Germany	—
30	Acyldepsipeptide antibiotics–current state of knowledge	Medical University of Warsaw	Poland	—

Showing the 30 most-cited of 49 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

Mass spectrometry methods for studying structure and dynamics of biological macromolecules

2014 · 185 citations (GS)

Field-normalised: 136 Semantic Scholar citations place it in the top 5% of Chemistry papers from 2014 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Collision induced unfolding of isolated proteins in the gas phase: past, present, and future	University of Michigan	United States	—
2	Ion activation methods for peptides and proteins	—	—	—
3	Surface-induced dissociation mass spectrometry as a structural biology tool	—	—	—
4	Revealing anisotropic growth of liraglutide oligomers by native ion mobility mass spectrometry and molecular dynamics simulation	—	—	—
5	Single-organelle localization-based super-resolution imaging for subcellular molecules microdynamics	Shandong First Medical University	China	—
6	Characterization of native protein complexes using ultraviolet photodissociation mass spectrometry	—	—	—
7	Going beyond electrospray: mass spectrometric studies of chemical reactions in and on liquids	Stanford University	United States	—
8	Microfluidic paper-based analytical devices for potential use in quantitative and direct detection of disease biomarkers in clinical analysis	University of Malaya	Malaysia	—
9	The advancement of chemical cross-linking and mass spectrometry for structural proteomics: from single proteins to protein interaction networks	—	—	—
10	Enhanced dissociation of intact proteins with high capacity electron transfer dissociation	—	—	—

No.	Citing paper	Citing institution(s)	Country	S2
11	Chimeric cellobiose dehydrogenases reveal the function of cytochrome domain mobility for the electron transfer to lytic polysaccharide monooxygenase	—	—	—
12	Polyphosphoinositide-binding domains: Insights from peripheral membrane and lipid-transfer proteins	—	—	—
13	Computational strategies and challenges for using native ion mobility mass spectrometry in biophysics and structural biology	King's College London, Weizmann Institute of Science	Israel, United Kingdom	—
14	Getting to the core of protein pharmaceuticals–comprehensive structure analysis by mass spectrometry	University of Copenhagen	Denmark	—
15	Impact of G12 mutations on the structure of K-Ras probed by ultraviolet photodissociation mass spectrometry	—	—	—
16	Charge detection mass spectrometry for the characterization of mass and surface area of composite nanoparticles	—	—	—
17	A review of the role of chemical modification methods in contemporary mass spectrometry-based proteomics research	ETH Zurich	Switzerland	—
18	Transition metal ion FRET in the gas phase: A 10–40 Å range molecular ruler for mass-selected biomolecular ions	—	—	—
19	Mass spectrometry beyond the native state	University of Oxford	United Kingdom	—
20	Single molecule-level detection via liposome-based signal amplification mass spectrometry counting assay	—	—	—
21	Biophysical characterization of proteins in developing biopharmaceuticals	—	—	—
22	Amphipols outperform dodecylmaltoside micelles in stabilizing membrane protein structure in the gas phase	—	—	—
23	Lysine conjugation properties in human IgGs studied by integrating high-resolution native mass spectrometry and bottom-up proteomics	—	—	—
24	Structural evaluation of protein/metal complexes via native electrospray ultraviolet photodissociation mass spectrometry	—	—	—
25	Recognition of human IgG1 by Fcγ receptors: structural insights from hydrogen–deuterium exchange and fast photochemical oxidation of proteins coupled with mass …	—	—	—
26	Introduction to mass spectrometry, a tutorial	Leiden University Medical Center, Vrije Universiteit Amsterdam	Netherlands	—

No.	Citing paper	Citing institution(s)	Country	S2
27	Using hydrogen deuterium exchange mass spectrometry to engineer optimized constructs for crystallization of protein complexes: Case study of PI4KIIIβ with Rab11	—	—	—
28	Laser desorption postionization mass spectrometry imaging of folic acid molecules in tumor tissue	—	—	—
29	Emerging native Orbitrap mass spectrometry for probing higher-order structures of proteins: Recent progress and applications	Beijing Institute of Technology, Chinese Academy of Inspection and Quarantine	China	—
30	Diethylpyrocarbonate footprints a membrane protein in micelles	Washington University	United States	—

Showing the 30 most-cited of 182 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

Effects of protein–ligand interactions on hydrogen/deuterium exchange kinetics: canonical and non-canonical scenarios

2014 · 70 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Revealing the structural dynamics and functional properties of class II lanthipeptide synthetases using mass spectrometry-based techniques	McGill University	Canada	—
2	Structural characterization of biotechnologically and medicinally important proteins.	Charles University	Czech Republic	—
3	Study of conformations and conformational changes of proteins using mass spectrometric methods.	Charles University	Czech Republic	—
4	Advances in hydrogen/deuterium exchange mass spectrometry and the pursuit of challenging biological systems	Northeastern University	United States	—
5	An overview of hydrogen deuterium exchange mass spectrometry (HDX-MS) in drug discovery	—	—	—
6	Contemporary hydrogen deuterium exchange mass spectrometry	York University	Canada	—
7	Simple and fast maximally deuterated control (maxD) preparation for hydrogen–deuterium exchange mass spectrometry experiments	Northeastern University	United States	—
8	Hydrogen-deuterium exchange mass spectrometry: a novel structural biology approach to structure, dynamics and interactions of proteins and their ...	Semmelweis University	Hungary	—

No.	Citing paper	Citing institution(s)	Country	S2
9	Applications of hydrogen/deuterium exchange MS from 2012 to 2014	Northeastern University	United States	—
10	Small molecule assembly agonist alters the dynamics of hepatitis B virus core protein dimer and capsid	—	—	—
11	Hydrogen deuterium exchange and other mass spectrometry-based approaches for epitope mapping	—	—	—
12	Development of a Thiol–ene Microfluidic Chip for Hydrogen/Deuterium Exchange Mass Spectrometry (HDX-MS)	—	—	—
13	Identification of a direct interaction between the Fab domains of IgG antibodies and human FcRn upon IgG-FcRn complex formation	—	—	—
14	Peptide-level interactions between proteins and small-molecule drug candidates by two hydrogen– deuterium exchange MS-based methods: the example of ...	—	—	—
15	Anti-CRISPR proteins function through thermodynamic tuning and allosteric regulation of CRISPR RNA-guided surveillance complex	Montana State University	United States	—
16	Combining Crystallography and Hydrogen–Deuterium Exchange to Study Galectin–Ligand Complexes	—	—	—
17	Allostery links hACE2 binding, pan-variant neutralisation and helical extension in the SARS-CoV-2 Spike protein	Icosagen (Estonia), Toronto Metropolitan University, York University	Canada, Estonia	—
18	Adsorption induced changes of human hemoglobin on ferric pyrophosphate nanoparticle surface probed by isotope exchange mass spectrometry: an implication on ...	—	—	—
19	An extended polyanion activation surface in insulin degrading enzyme	University of Bristol, University of California, San Diego	United Kingdom, United States	—
20	Chemical Synthesis and Structure–Activity Relationship Studies of the Coagulation Factor Xa Inhibitor Tick Anticoagulant Peptide from the Hematophagous ...	University of Padua	Italy	—
21	The Utility Of Hydrogen Deuterium Exchange Mass Spectrometry For Characterization Of Proteins And Their Interactions.	University of Kansas	United States	—
22	Hydrogen-deuterium exchange mass spectrometry reveals three unique binding responses of mAbs directed to the catalytic domain of hCAIX	—	—	—
23	Using hydrogen/deuterium exchange mass spectrometry to understand bacterial membrane efflux proteins	King's College London, University of Southampton	United Kingdom	—

No.	Citing paper	Citing institution(s)	Country	S2
24	Ion mobility spectrometry-hydrogen deuterium exchange mass spectrometry of anions: Part 3. Estimating surface area exposure by deuterium uptake	—	—	—
25	Probing the conformational dynamics of affinity-enhanced T cell receptor variants upon binding the peptide-bound major histocompatibility complex by Hydrogen ...	—	—	—
26	Application of differential hydrogen exchange mass spectrometry in small molecule drug discovery	Scripps Research Institute	United States	—
27	Examining the role of structural dynamics in the assembly and function of the multidrug efflux pump AcrAB-TolC	King's College London	United Kingdom	—
28	Structural Interpretation of Hydrogen-Deuterium Exchange with Maximum-Entropy Simulation Reweighting	National Heart Lung and Blood Institute, National Institute of Neurological Disorders and Stroke	United States	—
29	Characterisation of Inhibitor Binding to the LEDGF/P75-Binding Domain of HIV-1 Integrase	University of the Witwatersrand	South Africa	—
30	Advances in Biochemistry & Applications in Medicine	—	—	—

Showing the 30 most-cited of 57 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 established a framework for distinguishing Type 1 and Type 2 scenarios in hydrogen exchange mass spectrometry studies of protein-ligand complexes, a method subsequently applied to characterize intrinsically disordered proteins.

The researcher's core contribution rests on the 2014 paper titled 'Type 1 and Type 2 scenarios in hydrogen exchange mass spectrometry studies on protein–ligand complexes.' This work appears to define a critical classification system for interpreting structural data in these complexes, providing a foundational reference for the field.

This line of work addresses the need for standardized interpretation in hydrogen exchange mass spectrometry. The subsequent 2016 paper, focusing on the conformational characterization of the intrinsically disordered protein Chibby, suggests the researcher extended this framework to analyze complex structural elements and target recognition in disordered systems, demonstrating the versatility of the initial methodological approach.

The significance of this contribution is evidenced by the core paper's 57 citations and the broader context of the researcher's work, where 90.4% of citing papers originate from independent researchers. This high degree of independent uptake indicates that the proposed scenarios have been widely adopted and trusted by the broader scientific community as a standard analytical tool.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 46

CORE PAPER

Type 1 and Type 2 scenarios in hydrogen exchange mass spectrometry studies on protein–ligand complexes

2014 · 57 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Using hydrogen deuterium exchange mass spectrometry to engineer optimized constructs for crystallization of protein complexes: Case study of PI4KIIIβ with Rab11	—	—	—
2	An overview of hydrogen deuterium exchange mass spectrometry (HDX-MS) in drug discovery	—	—	—
3	Characterisation of Inhibitor Binding to the LEDGF/P75-Binding Domain of HIV-1 Integrase	University of the Witwatersrand	South Africa	—
4	Mass spectrometry-based protein footprinting for higher-order structure analysis: fundamentals and applications	Washington University in St. Louis	United States	—
5	Hydrogen deuterium exchange mass spectrometry in biopharmaceutical discovery and development–A review	York University	Canada	—
6	Defining a canonical ligand-binding pocket in the orphan nuclear receptor Nurr1	Scripps Research Institute, University of Cincinnati	United States	—
7	Mapping of the allosteric site in cholesterol hydroxylase CYP46A1 for efavirenz, a drug that stimulates enzyme activity	Case Western Reserve University, National Institute of Standards and Technology	United States	—
8	Interdomain electron transfer in cellobiose dehydrogenase is governed by surface electrostatics	BOKU University, Czech Academy of Sciences, Institute of Microbiology, Université de Strasbourg	Austria, Czech Republic, France	—
9	Innate Conformational Dynamics Drive Binding Specificity in Anti-Apoptotic Proteins Mcl-1 and Bcl-2	The University of Chicago, University of Chicago, York University	Canada, United States	—
10	Structural insight into the calcium ion modulated interdomain electron transfer in cellobiose dehydrogenase	BOKU University, Czech Academy of Sciences, Institute of Microbiology	Austria, Czech Republic	—
11	A unique conformational distortion mechanism drives lipocalin 2 binding to bacterial siderophores	—	—	—
12	The interaction between the natural metalloendopeptidase inhibitor BJ46a and its target toxin jararhagin analyzed by structural mass spectrometry and molecular …	Fundação Oswaldo Cruz	Brazil	—
13	Multiple ligand-bound states of a phosphohexomutase revealed by principal component analysis of NMR peak shifts	—	—	—
14	Protein footprinting by mass spectrometry: H/D exchange, specific amino acid labeling, and fast photochemical oxidation of proteins	Washington University in St. Louis	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
15	Elucidating the Conformational Dynamics of YTH Domain Containing Family of Proteins	York University	Canada	—
16	Establishing structural characterization of noroviruses by hydrogen-deuterium exchange mass spectrometry (HDX-MS)	Netherlands Metabolomics Centre	Netherlands	—
17	Allosteric Relay Propagation in Nucleotide Binding Proteins Through Integrative Nodes	National University of Singapore	Singapore	—
18	Structural mass spectrometry goes viral (2019)	European X-ray Free-Electron Laser, Leibniz Institute of Virology (LIV)	Germany	—
19	Study of conformations and conformational changes of proteins using mass spectrometric methods. (2016)	Charles University	Czech Republic	—
20	Hydrogen-deuterium exchange mass spectrometry reveals three unique binding responses of mAbs directed to the catalytic domain of hCAIX (2021)	—	—	—
21	The Utility Of Hydrogen Deuterium Exchange Mass Spectrometry For Characterization Of Proteins And Their Interactions. (2024)	University of Kansas	United States	—
22	Identification of lead molecules for the development of antivirals targeting the Ebola virus matrix protein VP40 (2022)	Philipps-Universität Marburg	Germany	—
23	Conformational analysis of complex protein states by hydrogen/deuterium exchange mass spectrometry (HDX-MS): Challenges and emerging solutions (2018)	University of Copenhagen	Denmark	—
24	ExMS2: an integrated solution for hydrogen–deuterium exchange mass spectrometry data analysis (2019)	University of Pennsylvania	United States	—
25	Surface accessibility and dynamics of macromolecular assemblies probed by covalent labeling mass spectrometry and integrative modeling (2017)	King's College London, King’s College London, Martin Luther University Halle-Wittenberg	Germany, United Kingdom	—
26	Hydrogen-deuterium exchange mass spectrometry to study protein complexes (2018)	Northeastern University	United States	—
27	Hydrogen-deuterium exchange mass spectrometry of membrane proteins in lipid nanodiscs (2019)	University of Washington	United States	—
28	Probing the dynamic regulation of peripheral membrane proteins using hydrogen deuterium exchange–MS (HDX–MS) (2015)	University of Geneva, University of Victoria	Canada, Switzerland	—
29	Hydrogen–deuterium exchange reveals long-range dynamical allostery in soybean lipoxygenase (2018)	QB3, University of California, Berkeley	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
30	HDX-MS reveals orthosteric and allosteric changes in apolipoprotein-D structural dynamics upon binding of progesterone (2019)	National University of Singapore, University of Wollongong	Australia, Singapore	—

Showing the 30 most-cited of 41 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

Conformational characterization of the intrinsically disordered protein Chibby: Interplay between structural elements in target recognition

2016 · 8 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Advances in hydrogen/deuterium exchange mass spectrometry and the pursuit of challenging biological systems	Northeastern University	United States	—
2	Examining DNA structures with in-droplet hydrogen/deuterium exchange mass spectrometry	West Virginia University	United States	—
3	Chasing tails: cathepsin-L improves structural analysis of histones by HX-MS	Broad Institute, National Institute of Standards and Technology	United States	—
4	downloaded from the King's Research Portal at https://kclpure. kcl. ac. uk/portal	King's College London	United Kingdom	—
5	Chasing Tails: Cathepsin-L Improves Structural Analysis of Histones by HX-MS*[S]	Broad Institute, National Institute of Standards and Technology	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).

Contribution 3

Claim — Contribution 3

The researcher critically evaluated electrospray sources and calibration protocols in traveling wave ion mobility spectrometry, establishing essential methodological standards for accurate protein structural analysis.

The researcher's contribution centers on a 2015 study that critically examined electrospray sources and calibration issues within traveling wave ion mobility spectrometry. This work appears to address fundamental methodological challenges in obtaining reliable protein structural data, offering a rigorous assessment of instrumental parameters that were previously under-scrutinized. By focusing on these technical foundations, the research suggests a necessary correction or refinement in how such spectrometry is applied to complex biological samples.

The originality of this line of work lies in its targeted critique of standard experimental setups. Rather than introducing a new instrument, the researcher appears to have identified and articulated specific calibration pitfalls inherent in electrospray sources. This conservative, methodological focus indicates a shift toward ensuring data integrity in structural proteomics, addressing a gap where instrumental artifacts might have been mistaken for biological features.

The significance of this contribution is evidenced by its sustained uptake in the scientific community. With 72 citations, the paper has served as a reference point for subsequent studies. Notably, 90.4% of the citing papers originate from independent researchers, suggesting that the findings have been widely adopted and trusted across different institutions. This high degree of independent citation underscores the work's role in establishing a shared methodological baseline for the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 53

CORE PAPER

Protein structural studies by traveling wave ion mobility spectrometry: a critical look at electrospray sources and calibration issues

2015 · 72 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Mass Spectrometric Studies on the Structure of Desolvated Biomolecular Ions	—	—	—
2	Gas-phase probes of kinetically trapped peptides	EPFL	Switzerland	—
3	Fundamentals of ion mobility spectrometry	Uppsala University	Sweden	—
4	Comparison of CCS values determined by traveling wave ion mobility mass spectrometry and drift tube ion mobility mass spectrometry	—	—	—
5	Optimizing native ion mobility Q-TOF in helium and nitrogen for very fragile noncovalent structures	—	—	—
6	Linear and differential ion mobility separations of middle-down proteoforms	—	—	—
7	Using collision cross section distributions to assess the distribution of collision cross section values	—	—	—
8	Polymers for traveling wave ion mobility spectrometry calibration	—	—	—
9	Replica exchange molecular dynamics study of the amyloid beta (11–40) trimer penetrating a membrane	KU Leuven	Belgium	—
10	U-Shaped mobility analyzer: a compact and high-Resolution counter-Flow Ion mobility spectrometer	—	—	—
11	Oligonucleotide anion adduct formation using negative ion electrospray ion-mobility mass spectrometry	—	—	—
12	Increasing ubiquitin ion resistance to unfolding in the gas phase using chloride adduction: preserving more "native-like" conformations despite collisional activation	—	—	—
13	Dueling electrospray implemented on a traveling-wave ion mobility/time-of-flight mass spectrometer: Towards a gas-phase workbench for structural biology	University of Indianapolis	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
14	Experimental determination of activation energies for covalent bond formation via ion/ion reactions and competing processes	University of Oregon	United States	—
15	Comparison of Partially Denatured Cytochrome c Structural Ensembles in Solution and Gas Phases Using Cross-Linking Mass Spectrometry	University of Indianapolis	United States	—
16	Modular calibrant sets for the structural analysis of nucleic acids by ion mobility spectrometry mass spectrometry	—	—	—
17	Gas-phase structure of polymer ions: Tying together theoretical approaches and ion mobility spectrometry	—	—	—
18	Small molecule-mediated inhibition of β-2-microglobulin-based amyloid fibril formation	University of Massachusetts Amherst	United States	—
19	Corona discharge electrospray ionization of formate-containing solutions enables in-source reduction of disulfide bonds	National Research Council Canada	Canada	—
20	Structural heterogeneity in the preamyloid oligomers of β-2-microglobulin	University of Massachusetts Amherst	United States	—
21	Can IM-MS Collision Cross Sections of Biomolecules Be Rationalized Using Collision Cross-Section Trends of Polydisperse Synthetic Homopolymers?	—	—	—
22	Determining collision cross-sections of aromatic compounds in crude oil by using aromatic compound mixture as calibration standard	—	—	—
23	PolycIMS: Polymers for Automated Cyclic Ion Mobility Spectrometry Calibration	University of Mons	Belgium	—
24	Mass Spectrometry Methods For Macromolecules: Polymer Architectures, Cross-Linking, and Surface Imaging	University of Akron	United States	—
25	The F19W mutation reduces the binding affinity of the transmembrane Aβ 11–40 trimer to the membrane bilayer	Duy Tan University, North Carolina State University	United States, Vietnam	—
26	CCS for Modelling 3D Structures	Durham University, Karolinska Institutet, King's College London	Sweden, United Kingdom	—
27	Reactivity at the membrane interface	Durham University	United Kingdom	—
28	Study of conformations and conformational changes of proteins using mass spectrometric methods.	Charles University	Czech Republic	—
29	Complete characterization of post-translationally modified isomeric peptides by linear and non-linear ion mobility, and tandem mass spectrometry	—	—	—
30	Experimental Techniques	Chatham University	United States	—

Showing the 30 most-cited of 53 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
Western University	Canada	THE 201–250 · QS 151	31
Northeastern University	United States	QS 384	16
York University	Canada	SCImago #1302 · THE 401–500 · QS 333	14
University of Toronto	Canada	SCImago #39 · THE 21 · QS 29	14
University of Guelph	Canada	SCImago #1566 · THE 401–500 · QS =504	11
The University of Texas at Austin	United States	THE 50 · QS 68	9
University of Copenhagen	Denmark	SCImago #177 · THE 90 · QS 101	8
King's College London	United Kingdom	THE 38 · QS 31	7
Charles University	Czech Republic	SCImago #797 · THE 401–500 · QS =265	7
University of Leeds	United Kingdom	SCImago #377 · THE 118 · QS 86	6
ETH Zurich	Switzerland	THE 11 · QS 7	6
La Trobe University	Australia	SCImago #1321 · THE 251–300 · QS =233	5
University of Saskatchewan	Canada	SCImago #1541 · THE 351–400 · QS 378	5
University of Wisconsin–Madison	United States	SCImago #174 · THE =53 · QS =110	5
National Institute of Standards and Technology	United States	SCImago #674	5

Geographic distribution of citing authors

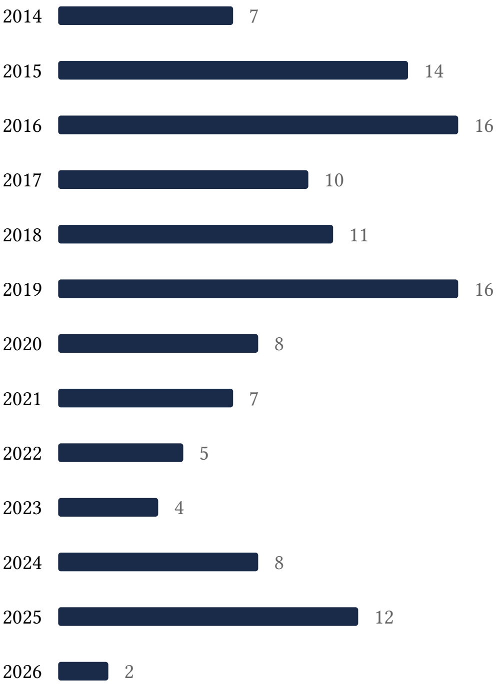
Country	Citing papers
United States	120
Canada	80
United Kingdom	27
Germany	18
China	14
France	13
Czech Republic	11
Switzerland	11
Denmark	10
Australia	10

Country	Citing papers
Italy	8
India	6

Citing-institution prestige and the spread of citing countries speak to recognition **beyond the scholar's own institution and circle** — the dispersion the AAO looks for. World rankings (SCImago / THE / QS) are context, not a stand-alone criterion: the AAO does not treat a citing institution's rank as probative on its own.

E. Citation Growth Over Time

Distinct citing papers by publication year. Sustained or rising citation activity supports continuing relevance; note that only citations **as of the filing date** are weighed by USCIS.



F. AAO Precedent Considerations

Pre-filing self-check (AAO denial patterns)

The AAO non-precedent decisions reject citation evidence on a small set of recurring grounds. Confirm the petition addresses each before filing:

- ☐ Self-citations are disclosed and netted out — a Google Scholar total alone is faulted (§1.1).
- ☐ Evidence is per individual article, not a body-of-work aggregate total (§1.2).
- ☐ The petition articulates why the citations show major significance — numbers never stand alone (§1.5).
- ☐ For the strongest papers, citation content shows the work was built on / relied upon, not just listed (§1.6, §2.2).
- ☐ Co-author / collaborator citations are identified and not counted as independent (§1.7).

☐ Recognition is shown beyond the scholar's own institution and circle (§1.8).
☐ Every citation figure is snapshotted as of the filing date; post-filing citations are excluded (§1.9).
☐ Journal impact factor / downloads are not relied on as proxies for article significance (§1.10, §1.12).
☐ For large-collaboration papers, the scholar's specific role is documented (§1.13).
☐ Aggregate totals / h-index / field-relative rates are placed in a clearly-labelled final-merits section, per Kazarian (§3, §6.1.7).

Disclaimer

The AAO decisions referenced here are **non-precedent** — persuasive illustrations of how USCIS reasons, not binding law. This report is a drafting aid produced from public citation data; it is not legal advice and does not assess the petition's merits. All analysis must be reviewed by qualified immigration counsel.

G. Citation Evidence Index

Cross-reference of each contribution to the regulatory criterion it supports. Counsel should map these to the petition's exhibit numbers.

Contribution	Core paper	Indep. cites	Supports
Contribution 1	Activation of ClpP protease by ADEP antibiotics: insights from hydrogen exchange mass spectrometry	288	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 2	Type 1 and Type 2 scenarios in hydrogen exchange mass spectrometry studies on protein–ligand complexes	46	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 3	Protein structural studies by traveling wave ion mobility spectrometry: a critical look at electrospray sources and calibration issues	53	8 CFR 204.5(i)(3) — Outstanding Researcher