Stephen J Valentine

List of Publications by Year
in descending order

95	5,454	87888 38	82547 72
papers	citations	h-index	g-index

98	98	98	2833
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Physicochemical Properties Altered by the Tail Group of Lipid Membranes Influence Huntingtin Aggregation and Lipid Binding. Journal of Physical Chemistry B, 2022, 126, 3067-3081.	2.6	6
2	Oxidation Promotes Distinct Huntingtin Aggregates in the Presence and Absence of Membranes. Biochemistry, 2022, 61, 1517-1530.	2.5	4
3	Vibrating Sharpâ€edge Spray Ionization (VSSI) for voltageâ€free direct analysis of samples using mass spectrometry. Rapid Communications in Mass Spectrometry, 2021, 35, e8232.	1.5	37
4	Physicochemical Property Correlations with Ionization Efficiency in Capillary Vibrating Sharp-Edge Spray Ionization (cVSSI). Journal of the American Society for Mass Spectrometry, 2021, 32, 84-94.	2.8	7
5	Lipid headgroups alter huntingtin aggregation on membranes. Biochimica Et Biophysica Acta - Biomembranes, 2021, 1863, 183497.	2.6	15
6	Protons Are Fast and Smart; Proteins Are Slow and Dumb: On the Relationship of Electrospray Ionization Charge States and Conformations. Journal of the American Society for Mass Spectrometry, 2021, 32, 1553-1561.	2.8	17
7	Characterizing Multidevice Capillary Vibrating Sharp-Edge Spray Ionization for In-Droplet Hydrogen/Deuterium Exchange to Enhance Compound Identification. ACS Omega, 2021, 6, 18370-18382.	3.5	8
8	Integrated sample desalting, enrichment, and ionization on an omniphobic glass slide for direct mass spectrometry analysis. Rapid Communications in Mass Spectrometry, 2021, 35, e9179.	1.5	3
9	Combining Field-Enabled Capillary Vibrating Sharp-Edge Spray Ionization with Microflow Liquid Chromatography and Mass Spectrometry to Enhance â€˜Omics Analyses. Journal of the American Society for Mass Spectrometry, 2021, 32, 473-485.	2.8	11
10	Nucleation Inhibition of Huntingtin Protein (htt) by Polyproline PPII Helices: A Potential Interaction with the N-Terminal Î±-Helical Region of Htt. Biochemistry, 2020, 59, 436-449.	2.5	14
11	Acetylation of AÎ²₄₀ Alters Aggregation in the Presence and Absence of Lipid Membranes. ACS Chemical Neuroscience, 2020, 11, 146-161.	3.5	11
12	Investigating the interactions of the first 17 amino acid residues of Huntingtin with lipid vesicles using mass spectrometry and molecular dynamics. Journal of Mass Spectrometry, 2020, 55, e4470.	1.6	10
13	Huntingtin Aggregation and Lipid Binding are Influenced by Physicochemical Properties of Membranes. Biophysical Journal, 2020, 118, 59a.	0.5	0
14	Facile Improvement of Negative Ion Mode Electrospray Ionization Using Capillary Vibrating Sharp-Edge Spray Ionization. Analytical Chemistry, 2020, 92, 2492-2502.	6.5	23
15	Recommendations for reporting ion mobility Mass Spectrometry measurements. Mass Spectrometry Reviews, 2019, 38, 291-320.	5.4	315
16	Hydrogen Peroxide Modifies Aβâ€“Membrane Interactions with Implications for Aβ₄₀ Aggregation. Biochemistry, 2019, 58, 2893-2905.	2.5	12
17	Synthetic Small Molecule Characterization and Isomer Discrimination Using Gas-Phase Hydrogenâ€“Deuterium Exchange IMS-MS. Analytical Chemistry, 2019, 91, 6259-6265.	6.5	4
18	Rapid Solution-Phase Hydrogen/Deuterium Exchange for Metabolite Compound Identification. Journal of the American Society for Mass Spectrometry, 2019, 30, 1102-1114.	2.8	11

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19	Capillary Vibrating Sharp-Edge Spray Ionization (cVSSI) for Voltage-Free Liquid Chromatography-Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2019, 30, 824-831.	2.8	33
20	Ion Mobility Spectrometry-Mass Spectrometry Coupled with Gas-Phase Hydrogen/Deuterium Exchange for Metabolomics Analyses. Journal of the American Society for Mass Spectrometry, 2018, 29, 230-241.	2.8	15
21	Magnifying ion mobility spectrometryâ€“mass spectrometry measurements for biomolecular structure studies. Current Opinion in Chemical Biology, 2018, 42, 101-110.	6.1	18
22	Comparison of Peptide Ion Conformers Arising from Non-Helical and Helical Peptides Using Ion Mobility Spectrometry and Gas-Phase Hydrogen/Deuterium Exchange. Journal of the American Society for Mass Spectrometry, 2018, 29, 2402-2412.	2.8	8
23	Comprehensive Peptide Ion Structure Studies Using Ion Mobility Techniques: Part 3. Relating Solution-Phase to Gas-Phase Structures. Journal of the American Society for Mass Spectrometry, 2018, 29, 1665-1677.	2.8	20
24	Ion Mobility, Hydrogen/Deuterium Exchange, and Isotope Scrambling: Tools to Aid Compound Identification in â€˜Omics Mixtures. Analytical Chemistry, 2017, 89, 6399-6407.	6.5	9
25	Comprehensive Peptide Ion Structure Studies Using Ion Mobility Techniques: Part 1. An Advanced Protocol for Molecular Dynamics Simulations and Collision Cross-Section Calculation. Journal of the American Society for Mass Spectrometry, 2017, 28, 947-959.	2.8	18
26	Comprehensive Gas-Phase Peptide Ion Structure Studies Using Ion Mobility Techniques: Part 2. Gas-Phase Hydrogen/Deuterium Exchange for Ion Population Estimation. Journal of the American Society for Mass Spectrometry, 2017, 28, 960-970.	2.8	11
27	Acetylation within the First 17 Residues of Huntingtin Exon 1 Alters Aggregation and Lipid Binding. Biophysical Journal, 2016, 111, 349-362.	0.5	55
28	Structural Assignments of Sulfur-Containing Compounds in Crude Oil Using Ion Mobility Spectrometry-Mass Spectrometry. Energy & Fuels, 2016, 30, 9150-9161.	5.1	18
29	Ion Mobility Spectrometry-Hydrogen Deuterium Exchange Mass Spectrometry of Anions: Part 3. Estimating Surface Area Exposure by Deuterium Uptake. Journal of the American Society for Mass Spectrometry, 2016, 27, 462-473.	2.8	10
30	Factors Modulating the Interaction of Huntingtin with Lipid Membranes: Implications for Huntington's Disease. Biophysical Journal, 2016, 110, 358a-359a.	0.5	0
31	Ion Mobility Spectrometry-Hydrogen Deuterium Exchange Mass Spectrometry of Anions: Part 2. Assessing Charge Site Location and Isotope Scrambling. Journal of the American Society for Mass Spectrometry, 2016, 27, 451-461.	2.8	10
32	Comparative plasma proteomic studies of pulmonary TiO2 nanoparticle exposure in rats using liquid chromatography tandem mass spectrometry. Journal of Proteomics, 2016, 130, 85-93.	2.4	13
33	Gas-Phase Hydrogen-Deuterium Exchange Labeling of Select Peptide Ion Conformer Types: a Per-Residue Kinetics Analysis. Journal of the American Society for Mass Spectrometry, 2015, 26, 1115-1127.	2.8	16
34	Lysine residues in the N-terminal huntingtin amphipathicÎ±-helix play a key role in peptide aggregation. Journal of Mass Spectrometry, 2015, 50, 117-126.	1.6	17
35	Ion Mobility Spectrometry-Hydrogen Deuterium Exchange Mass Spectrometry of Anions: Part 1. Peptides to Proteins. Journal of the American Society for Mass Spectrometry, 2015, 26, 564-576.	2.8	24
36	Huntingtin N-Terminal Monomeric and Multimeric Structures Destabilized by Covalent Modification of Heteroatomic Residues. Biochemistry, 2015, 54, 4285-4296.	2.5	28

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37	Online Deuterium Hydrogen Exchange and Protein Digestion Coupled with Ion Mobility Spectrometry and Tandem Mass Spectrometry. Analytical Chemistry, 2015, 87, 5247-5254.	6.5	10
38	Advances in ion mobility-mass spectrometry instrumentation and techniques for characterizing structural heterogeneity. Analyst, The, 2015, 140, 6782-6798.	3.5	27
39	Combining Ion Mobility Spectrometry with Hydrogen-Deuterium Exchange and Top-Down MS for Peptide Ion Structure Analysis. Journal of the American Society for Mass Spectrometry, 2014, 25, 2103-2115.	2.8	39
40	A New Ion Mobilityâ€"Linear Ion Trap Instrument for Complex Mixture Analysis. Analytical Chemistry, 2014, 86, 8121-8128.	6.5	32
41	A Database of Alkaline-Earth-Coordinated Peptide Cross Sections: Insight into General Aspects of Structure. Journal of the American Society for Mass Spectrometry, 2013, 24, 768-779.	2.8	19
42	Overtone Mobility Spectrometry: Part 5. Simulations and Analytical Expressions Describing Overtone Limits. Journal of the American Society for Mass Spectrometry, 2013, 24, 615-621.	2.8	9
43	Oscillations of Chiral Preference in Proline Clusters. Journal of Physical Chemistry A, 2013, 117, 1035-1041.	2.5	16
44	Mannose7 Glycan Isomer Characterization by IMS-MS/MS Analysis. Journal of the American Society for Mass Spectrometry, 2012, 23, 2158-2166.	2.8	63
45	Conformation Types of Ubiquitin [M+8H]8+ Ions from Water:Methanol Solutions: Evidence for the N and A States in Aqueous Solution. Journal of Physical Chemistry B, 2012, 116, 3344-3352.	2.6	87
46	Collisional Activation of [14Pro+2H]²⁺ Clusters: Chiral Dependence of Evaporation and Fission Processes. Journal of Physical Chemistry B, 2012, 116, 7644-7651.	2.6	7
47	Chirality and Packing in Small Proline Clusters. Journal of Physical Chemistry B, 2012, 116, 11442-11446.	2.6	12
48	Extracted fragment ion mobility distributions: A new method for complex mixture analysis. International Journal of Mass Spectrometry, 2012, 309, 154-160.	1.5	40
49	Analyzing a mixture of disaccharides by IMS-VUVPD-MS. International Journal of Mass Spectrometry, 2012, 309, 161-167.	1.5	61
50	Number of Solution States of Bradykinin from Ion Mobility and Mass Spectrometry Measurements. Journal of the American Chemical Society, 2011, 133, 13810-13813.	13.7	142
51	Controlled Formation of Peptide Bonds in the Gas Phase. Journal of the American Chemical Society, 2011, 133, 15834-15837.	13.7	30
52	Using Ion Mobility Data to Improve Peptide Identification: Intrinsic Amino Acid Size Parameters. Journal of Proteome Research, 2011, 10, 2318-2329.	3.7	58
53	Overtone Mobility Spectrometry: Part 3. On the Origin of Peaks. Journal of the American Society for Mass Spectrometry, 2011, 22, 804-816.	2.8	19
54	An Ion Mobility/Ion Trap/Photodissociation Instrument for Characterization of Ion Structure. Journal of the American Society for Mass Spectrometry, 2011, 22, 1477-85.	2.8	72

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55	A Scanning Frequency Mode for Ion Cyclotron Mobility Spectrometry. Analytical Chemistry, 2010, 82, 8266-8271.	6.5	38
56	Gas-phase conformation-specific photofragmentation of proline-containing peptide ions. Journal of the American Society for Mass Spectrometry, 2010, 21, 1455-1465.	2.8	30
57	Evidence for a Quasi-Equilibrium Distribution of States for Bradykinin [M + 3H]³⁺ Ions in the Gas Phase. Journal of Physical Chemistry B, 2010, 114, 7777-7783.	2.6	84
58	Determination of Cross Sections by Overtone Mobility Spectrometry: Evidence for Loss of Unstable Structures at Higher Overtones. Journal of Physical Chemistry B, 2010, 114, 12406-12415.	2.6	32
59	Overtone mobility spectrometry: Part 1. Experimental observations. Journal of the American Society for Mass Spectrometry, 2009, 20, 729-737.	2.8	70
60	Protein oligomers frozen in time. Nature Chemistry, 2009, 1, 257-258.	13.6	11
61	Developing IMSâ€“IMSâ€“MS for rapid characterization of abundant proteins in human plasma. International Journal of Mass Spectrometry, 2009, 283, 149-160.	1.5	34
62	Overtone mobility spectrometry: Part 2. Theoretical considerations of resolving power. Journal of the American Society for Mass Spectrometry, 2009, 20, 738-750.	2.8	44
63	Treatise on the Measurement of Molecular Masses with Ion Mobility Spectrometry. Analytical Chemistry, 2009, 81, 5876-5880.	6.5	26
64	Towards a systems level analysis of health and nutrition. Current Opinion in Biotechnology, 2008, 19, 100-109.	6.6	38
65	Improving the Efficiency of IMSâ^'IMS by a Combing Technique. Analytical Chemistry, 2008, 80, 1918-1927.	6.5	26
66	Mapping the human plasma proteome by SCX-LC-IMS-MS. Journal of the American Society for Mass Spectrometry, 2007, 18, 1249-1264.	2.8	171
67	Toward Plasma Proteome Profiling with Ion Mobility-Mass Spectrometry. Journal of Proteome Research, 2006, 5, 2977-2984.	3.7	139
68	Coupling Desorption Electrospray Ionization with Ion Mobility/Mass Spectrometry for Analysis of Protein Structure:Â Evidence for Desorption of Folded and Denatured States. Journal of Physical Chemistry B, 2006, 110, 5045-5051.	2.6	116
69	An IMSâ^'IMS Analogue of MSâ^'MS. Analytical Chemistry, 2006, 78, 4161-4174.	6.5	251
70	Split-Field Drift Tube/Mass Spectrometry and Isotopic Labeling Techniques for Determination of Single Amino Acid Polymorphisms. Journal of Proteome Research, 2006, 5, 1879-1887.	3.7	9
71	IMSâ^'IMS and IMSâ^'IMSâ^'IMS/MS for Separating Peptide and Protein Fragment Ions. Analytical Chemistry, 2006, 78, 2802-2809.	6.5	183
72	Developing liquid chromatography ion mobility mass spectometry techniques. Expert Review of Proteomics, 2005, 2, 553-565.	3.0	61

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73	Development of Field Modulation in a Split-Field Drift Tube for High-Throughput Multidimensional Separations. Journal of Proteome Research, 2005, 4, 25-35.	3.7	29
74	Proteome Profiling for Assessing Diversity:Â Analysis of Individual Heads ofDrosophilamelanogasterUsing LCâ^'Ion Mobilityâ^'MS. Journal of Proteome Research, 2005, 4, 1238-1247.	3.7	45
75	Mapping the Proteome ofDrosophilamelanogaster:Â Analysis of Embryos and Adult Heads by LCâ^'IMSâ^'MS Methods. Journal of Proteome Research, 2005, 4, 1223-1237.	3.7	65
76	Nanoflow LC/IMS-MS and LC/IMS-CID/MS of protein mixtures. Journal of the American Society for Mass Spectrometry, 2004, 15, 1341-1353.	2.8	38
77	A Split-Field Drift Tube for Separation and Efficient Fragmentation of Biomolecular Ions. Analytical Chemistry, 2003, 75, 6202-6208.	6.5	67
78	Development of High-Sensitivity Ion Trap Ion Mobility Spectrometry Time-of-Flight Techniques:Â A High-Throughput Nano-LC-IMS-TOF Separation of Peptides Arising from aDrosophilaProtein Extract. Analytical Chemistry, 2003, 75, 5137-5145.	6.5	111
79	Resolving Isomeric Peptide Mixtures:Â A Combined HPLC/Ion Mobility-TOFMS Analysis of a 4000-Component Combinatorial Library. Analytical Chemistry, 2002, 74, 26-36.	6.5	95
80	Development of high-throughput liquid chromatography injected ion mobility quadrupole time-of-flight techniques for analysis of complex peptide mixtures. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2002, 782, 343-351.	2.3	29
81	Temperature-dependent H/D exchange of compact and elongated cytochrome c ions in the gas phase. Journal of the American Society for Mass Spectrometry, 2002, 13, 506-517.	2.8	79
82	Multidimensional separations of complex peptide mixtures: a combined high-performance liquid chromatography/ion mobility/time-of-flight mass spectrometry approach. International Journal of Mass Spectrometry, 2001, 212, 97-109.	1.5	133
83	A database of 660 peptide ion cross sections: Use of intrinsic size parameters for bona fide predictions of cross sections. Journal of the American Society for Mass Spectrometry, 1999, 10, 1188-1211.	2.8	191
84	ESI/Ion Trap/Ion Mobility/Time-of-Flight Mass Spectrometry for Rapid and Sensitive Analysis of Biomolecular Mixtures. Analytical Chemistry, 1999, 71, 291-301.	6.5	193
85	Intrinsic Amino Acid Size Parameters from a Series of 113 Lysine-Terminated Tryptic Digest Peptide Ions. Journal of Physical Chemistry B, 1999, 103, 1203-1207.	2.6	70
86	High-order structure and dissociation of gaseous peptide aggregates that are hidden in mass spectra. Journal of the American Society for Mass Spectrometry, 1998, 9, 743-759.	2.8	141
87	Gas-phase separations of protease digests. Journal of the American Society for Mass Spectrometry, 1998, 9, 1213-1216.	2.8	104
88	Three-Dimensional Ion Mobility/TOFMS Analysis of Electrosprayed Biomolecules. Analytical Chemistry, 1998, 70, 2236-2242.	6.5	330
89	Peer Reviewed: Injected-Ion Mobility Analysis of Biomolecules. Analytical Chemistry, 1997, 69, 728A-735A.	6.5	45
90	Disulfide-Intact and -Reduced Lysozyme in the Gas Phase:Â Conformations and Pathways of Folding and Unfolding. Journal of Physical Chemistry B, 1997, 101, 3891-3900.	2.6	224

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91	H/D Exchange Levels of Shape-Resolved Cytochrome c Conformers in the Gas Phase. Journal of the American Chemical Society, 1997, 119, 3558-3566.	13.7	192
92	An Ion Trap Interface for ESIâ^'Ion Mobility Experiments. Analytical Chemistry, 1997, 69, 4156-4161.	6.5	112
93	Conformer-dependent proton-transfer reactions of ubiquitin ions. Journal of the American Society for Mass Spectrometry, 1997, 8, 954-961.	2.8	219
94	Development of cVSSI-APCI for the Improvement of Ion Suppression and Matrix Effects in Complex Mixtures. Analytical Chemistry, 0, , .	6.5	4
95	Rapid and flexible onâ€line desalting using Nafion coated melamine sponge for mass spectrometry analysis. Rapid Communications in Mass Spectrometry, 0, , .	1.5	1