

# Michael A Freitas

## List of Publications by Year in descending order

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131  
papers

5,459  
citations

81889

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138  
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138  
docs citations

138  
times ranked

7381  
citing authors

#	ARTICLE	IF	CITATIONS
1	The functional impact of BRCA1 BRCT domain variants using multiplexed DNA double-strand break repair assays. American Journal of Human Genetics, 2022, 109, 618-630.	6.2	8
2	Techniques for estimating genetically variable peptides and semi-continuous likelihoods from massively parallel sequencing data. Forensic Science International: Genetics, 2022, 59, 102719.	3.1	2
3	TIMSCONVERT: a workflow to convert trapped ion mobility data to open data formats. Bioinformatics, 2022, 38, 4046-4047.	4.1	1
4	Fractionation of DNA and protein from individual latent fingerprints for forensic analysis. Forensic Science International: Genetics, 2021, 50, 102405.	3.1	9
5	Multiple Imputation Approaches Applied to the Missing Value Problem in Bottom-Up Proteomics. International Journal of Molecular Sciences, 2021, 22, 9650.	4.1	20
6	Detection of single peptide with only one amino acid modification via electronic fingerprinting using reengineered durable channel of Phi29 DNA packaging motor. Biomaterials, 2021, 276, 121022.	11.4	12
7	Optimization of proteomics sample preparation for forensic analysis of skin samples. Journal of Proteomics, 2021, 249, 104360.	2.4	4
8	Epigenetic regulation of nuclear lamina-associated heterochromatin by HAT1 and the acetylation of newly synthesized histones. Nucleic Acids Research, 2021, 49, 12136-12151.	14.5	14
9	Proteomic characterization of a trauma-based rat model of heterotopic ossification identifies interactive signaling networks as potential therapeutic targets. Journal of Proteomics, 2020, 226, 103907.	2.4	1
10	Tagging enhances histochemical and biochemical detection of Ran Binding Protein 9 in vivo and reveals its interaction with Nucleolin. Scientific Reports, 2020, 10, 7138.	3.3	4
11	Histone acetyltransferase 1 is required for DNA replication fork function and stability. Journal of Biological Chemistry, 2020, 295, 8363-8373.	3.4	23
12	An algorithm for random match probability calculation from peptide sequences. Forensic Science International: Genetics, 2020, 47, 102295.	3.1	4
13	Isolation of Proteins on Nascent Chromatin and Characterization by Quantitative Mass Spectrometry. Methods in Molecular Biology, 2019, 1983, 17-27.	0.9	2
14	A Microfluidic Chip Enables Isolation of Exosomes and Establishment of Their Protein Profiles and Associated Signaling Pathways in Ovarian Cancer. Cancer Research, 2019, 79, 3503-3513.	0.9	72
15	The long non-coding RNA HOXB-AS3 regulates ribosomal RNA transcription in NPM1-mutated acute myeloid leukemia. Nature Communications, 2019, 10, 5351.	12.8	71
16	Middleâ€Down Characterization of the Cell Cycle Dependence of Histone H4 Posttranslational Modifications and Proteoforms. Proteomics, 2018, 18, e1700442.	2.2	31
17	The proinflammatory protein HMGB1 is a substrate of transglutaminase-2 and forms high-molecular weight complexes with autoantigens. Journal of Biological Chemistry, 2018, 293, 8394-8409.	3.4	17
18	Trauma induced heterotopic ossification patient serum alters mitogen activated protein kinase signaling in adipose stem cells. Journal of Cellular Physiology, 2018, 233, 7035-7044.	4.1	12

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19	Abstract 3335: Characterizing the MAXH28Rsecretome in endometrial cancer. , 2018, , .		0
20	Abstract 1285: Deep mutagenesis analysis on BRCA1 variants in high throughput DNA repair assays. , 2018, , .		0
21	Abstract 1367: BRCA1 and BARD1 protein interactions that are required for DNA repair function. , 2018, , .		0
22	The impact of cruciferous vegetable isothiocyanates on histone acetylation and histone phosphorylation in bladder cancer. Journal of Proteomics, 2017, 156, 94-103.	2.4	49
23	Nitric oxide mediated inhibition of antigen presentation from DCs to CD4+ T cells in cancer and measurement of STAT1 nitration. Scientific Reports, 2017, 7, 15424.	3.3	68
24	Identification of multiple roles for histone acetyltransferase 1 in replication-coupled chromatin assembly. Nucleic Acids Research, 2017, 45, 9319-9335.	14.5	37
25	A multi-model statistical approach for proteomic spectral count quantitation. Journal of Proteomics, 2016, 144, 23-32.	2.4	20
26	Tag-Count Analysis of Large-Scale Proteomic Data. Journal of Proteome Research, 2016, 15, 4742-4746.	3.7	7
27	Identification of replication-dependent and replication-independent linker histone complexes: Tpr specifically promotes replication-dependent linker histone stability. BMC Biochemistry, 2016, 17, 18.	4.4	9
28	MicroRNA regulation of stem cell differentiation and diseases of the bone and adipose tissue: Perspectives on miRNA biogenesis and cellular transcriptome. Biochimie, 2016, 124, 98-111.	2.6	64
29	Proteomic characterization of circulating extracellular vesicles identifies novel serum myeloma associated markers. Journal of Proteomics, 2016, 136, 89-98.	2.4	68
30	Quantitative Mass Spectrometry Reveals that Intact Histone H1 Phosphorylations are Variant Specific and Exhibit Single Molecule Hierarchical Dependence. Molecular and Cellular Proteomics, 2016, 15, 818-833.	3.8	29
31	The potential diagnostic power of extracellular vesicle analysis for multiple myeloma. Expert Review of Molecular Diagnostics, 2016, 16, 277-284.	3.1	10
32	Proteomic Signatures of Thymomas. PLoS ONE, 2016, 11, e0166494.	2.5	9
33	Proteomic profiling identifies specific histone species associated with leukemic and cancer cells. Clinical Proteomics, 2015, 12, 22.	2.1	18
34	Spinal Muscular Atrophy Biomarker Measurements from Blood Samples in a Clinical Trial of Valproic Acid in Ambulatory Adults. Journal of Neuromuscular Diseases, 2015, 2, 119-130.	2.6	13
35	The chromatin scaffold protein SAFB1 localizes SUMO-1 to the promoters of ribosomal protein genes to facilitate transcription initiation and splicing. Nucleic Acids Research, 2015, 43, 3605-3613.	14.5	27
36	The non-canonical hydroxylase structure of YfcM reveals a metal ion-coordination motif required for EF-P hydroxylation. Nucleic Acids Research, 2014, 42, 12295-12305.	14.5	15

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37	SILAC Peptide Ratio Calculator: A Tool for SILAC Quantitation of Peptides and Post-Translational Modifications. Journal of Proteome Research, 2014, 13, 506-516.	3.7	4
38	Histone H1 Phosphorylation in Breast Cancer. Journal of Proteome Research, 2014, 13, 2453-2467.	3.7	38
39	8: Epigenetics and microRNA as a unifying mechanism in severe preeclampsia. American Journal of Obstetrics and Gynecology, 2014, 210, S5.	1.3	1
40	Biological aging alters circadian mechanisms in murine adipose tissue depots. Age, 2013, 35, 533-547.	3.0	17
41	Sites of Acetylation on Newly Synthesized Histone H4 Are Required for Chromatin Assembly and DNA Damage Response Signaling. Molecular and Cellular Biology, 2013, 33, 3286-3298.	2.3	26
42	Isolation and analysis of linker histones across cellular compartments. Journal of Proteomics, 2013, 91, 595-604.	2.4	12
43	Characterization of Multiple Myeloma Vesicles by Label-Free Relative Quantitation. Proteomics, 2013, 13, n/a-n/a.	2.2	32
44	Specificity Profiling of Dual Specificity Phosphatase Vaccinia VH1-related (VHR) Reveals Two Distinct Substrate Binding Modes*. Journal of Biological Chemistry, 2013, 288, 6498-6510.	3.4	14
45	Methylation of the PTPRO gene in human hepatocellular carcinoma and identification of VCP as its substrate. Journal of Cellular Biochemistry, 2013, 114, 1810-1818.	2.6	19
46	Alterations of Histone H1 Phosphorylation During Bladder Carcinogenesis. Journal of Proteome Research, 2013, 12, 3317-3326.	3.7	34
47	Discovery of Histone Modification Crosstalk Networks by Stable Isotope Labeling of Amino Acids in Cell Culture Mass Spectrometry (SILAC MS). Molecular and Cellular Proteomics, 2013, 12, 2048-2059.	3.8	33
48	H1 histones: current perspectives and challenges. Nucleic Acids Research, 2013, 41, 9593-9609.	14.5	188
49	Increasing the complexity of chromatin: functionally distinct roles for replication-dependent histone H2A isoforms in cell proliferation and carcinogenesis. Nucleic Acids Research, 2013, 41, 9284-9295.	14.5	25
50	In vivo NCL targeting affects breast cancer aggressiveness through miRNA regulation. Journal of Experimental Medicine, 2013, 210, 951-968.	8.5	121
51	In vivo NCL targeting affects breast cancer aggressiveness through miRNA regulation. Journal of Cell Biology, 2013, 201, i4-i4.	5.2	0
52	Abstract 1122: In vivo NCL-targeting affects breast cancer aggressiveness through miRNA regulation., 2013, .		0
53	Tcl1 protein functions as an inhibitor of de novo DNA methylation in B-cell chronic lymphocytic leukemia (CLL). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2555-2560.	7.1	58
54	Characterization of glomerular diseases using proteomic analysis of laser capture microdissected glomeruli. Modern Pathology, 2012, 25, 709-721.	5.5	57

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55	Using ontology-based methods for implementing role-based access control in cooperative systems. , 2012, , .		5
56	A quantitative proteomic workflow for characterization of frozen clinical biopsies: Laser capture microdissection coupled with label-free mass spectrometry. Journal of Proteomics, 2012, 77, 433-440.	2.4	38
57	Using Semantic Web Technologies for RBAC in Project-Oriented Environments. , 2012, , .		1
58	Apigenin induces DNA damage through the PKC $\delta$ -dependent activation of ATM and H2AX causing down-regulation of genes involved in cell cycle control and DNA repair. Biochemical Pharmacology, 2012, 84, 1571-1580.	4.4	46
59	Proteomic Analysis Reveals New Cardiac-Specific Dystrophin-Associated Proteins. PLoS ONE, 2012, 7, e43515.	2.5	72
60	Tetraspanin CD37 Directly Mediates Transduction of Survival and Apoptotic Signals. Cancer Cell, 2012, 21, 694-708.	16.8	122
61	Abstract 1351: Analysis of the in vivo tumor suppressive potential of PTPROt (truncated protein) Tj ETQq1 1 0.784314 rgBT /Overlock 1		
62	A Cloud-based Dynamic Workflow for Mass Spectrometry Data Analysis. , 2011, , .		14
63	Peptide-Based Inhibition of NF- $\kappa$ B Rescues Diaphragm Muscle Contractile Dysfunction in a Murine Model of Duchenne Muscular Dystrophy. Molecular Medicine, 2011, 17, 508-515.	4.4	51
64	Age-related changes in mesenchymal stem cells derived from rhesus macaque bone marrow. Aging Cell, 2011, 10, 66-79.	6.7	142
65	High-sensitivity TFA-free LC-MS for profiling histones. Proteomics, 2011, 11, 3326-3334.	2.2	10
66	A Dynamic Noise Level Algorithm for Spectral Screening of Peptide MS/MS Spectra. BMC Bioinformatics, 2010, 11, 436.	2.6	19
67	Unambiguous determination of isobaric histone modifications by reversed-phase retention time and high-mass accuracy. Analytical Biochemistry, 2010, 396, 13-22.	2.4	19
68	Assaying pharmacodynamic endpoints with targeted therapy: Flavopiridol and 17AAG induced dephosphorylation of histone H1.5 in acute myeloid leukemia. Proteomics, 2010, 10, 4281-4292.	2.2	13
69	Database Search Algorithm for Identification of Intact Cross-Links in Proteins and Peptides Using Tandem Mass Spectrometry. Journal of Proteome Research, 2010, 9, 3384-3393.	3.7	72
70	The Novel Deacetylase Inhibitor AR-42 Demonstrates Pre-Clinical Activity in B-Cell Malignancies In Vitro and In Vivo. PLoS ONE, 2010, 5, e10941.	2.5	49
71	Automated diagnosis of LC-MS/MS performance. Bioinformatics, 2009, 25, 1341-1343.	4.1	20
72	MassMatrix: A database search program for rapid characterization of proteins and peptides from tandem mass spectrometry data. Proteomics, 2009, 9, 1548-1555.	2.2	167

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73	A hierarchical MS <sup>2</sup> /MS <sup>3</sup> database search algorithm for automated analysis of phosphopeptide tandem mass spectra. <i>Proteomics</i> , 2009, 9, 1763-1770.	2.2	13
74	Validation of an LC-MS based approach for profiling histones in chronic lymphocytic leukemia. <i>Proteomics</i> , 2009, 9, 1197-1206.	2.2	22
75	Enrichment and characterization of histones by two-dimensional hydroxyapatite/reversed-phase liquid chromatography-mass spectrometry. <i>Analytical Biochemistry</i> , 2009, 388, 47-55.	2.4	9
76	Mass Spectrometry Profiles Superoxide-Induced Intramolecular Disulfide in the FMN-Binding Subunit of Mitochondrial Complex I. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 1875-1886.	2.8	13
77	A robust linear regression based algorithm for automated evaluation of peptide identifications from shotgun proteomics by use of reversed-phase liquid chromatography retention time. <i>BMC Bioinformatics</i> , 2008, 9, 347.	2.6	44
78	Monte Carlo Simulation-Based Algorithms for Analysis of Shotgun Proteomic Data. <i>Journal of Proteome Research</i> , 2008, 7, 2605-2615.	3.7	41
79	Identification and Characterization of Disulfide Bonds in Proteins and Peptides from Tandem MS Data by Use of the MassMatrix MS/MS Search Engine. <i>Journal of Proteome Research</i> , 2008, 7, 138-144.	3.7	123
80	Identification of Histone Demethylases in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 14262-14271.	3.4	96
81	Quantitative profiling of histone post-translational modifications by stable isotope labeling. <i>Methods</i> , 2007, 41, 312-319.	3.8	22
82	Histone H3-K56 Acetylation Is Catalyzed by Histone Chaperone-Dependent Complexes. <i>Molecular Cell</i> , 2007, 25, 703-712.	9.7	268
83	Mass spectrometry-based strategies for characterization of histones and their post-translational modifications. <i>Expert Review of Proteomics</i> , 2007, 4, 211-225.	3.0	38
84	Histone H4 N-Terminal Acetylation in Kasumi-1 Cells Treated with Depsipeptide Determined by Acetic Acid-Urea Polyacrylamide Gel Electrophoresis, Amino Acid Coded Mass Tagging, and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 81-88.	3.7	20
85	Histone H4 acetylation dynamics determined by stable isotope labeling with amino acids in cell culture and mass spectrometry. <i>Analytical Biochemistry</i> , 2007, 363, 22-34.	2.4	19
86	Liquid chromatography mass spectrometry profiling of histones. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2007, 850, 440-454.	2.3	29
87	Simultaneous metabolic labeling of cells with multiple amino acids: Localization and dynamics of histone acetylation and methylation. <i>Proteomics - Clinical Applications</i> , 2007, 1, 130-142.	1.6	4
88	A mass accuracy sensitive probability based scoring algorithm for database searching of tandem mass spectrometry data. <i>BMC Bioinformatics</i> , 2007, 8, 133.	2.6	127
89	Peptide mass mapping of acetylated isoforms of histone H4 from mouse lymphosarcoma cells treated with histone deacetylase (HDACs) inhibitors. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 1641-1653.	2.8	37
90	Histone H4 Lysine 91 Acetylation. <i>Molecular Cell</i> , 2005, 18, 123-130.	9.7	155

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91	Application of mass spectrometry to the identification and quantification of histone post-translational modifications. <i>Journal of Cellular Biochemistry</i> , 2004, 92, 691-700.	2.6	125
92	Comparison of peptide mass mapping and electron capture dissociation as assays for histone posttranslational modifications. <i>International Journal of Mass Spectrometry</i> , 2004, 234, 213-225.	1.5	29
93	Differential expression of histone post-translational modifications in acute myeloid and chronic lymphocytic leukemia determined by high-pressure liquid chromatography and mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 77-86.	2.8	59
94	Identification of novel histone post-translational modifications by peptide mass fingerprinting. <i>Chromosoma</i> , 2003, 112, 77-86.	2.2	244
95	Tool command language automation of the modular ion cyclotron data acquisition system (MIDAS) for data-dependent tandem Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 363-370.	1.5	12
96	High resolution electrospray ionization mass spectrometry and 2D solution NMR for the analysis of DOM extracted by C18 solid phase disk. <i>Organic Geochemistry</i> , 2003, 34, 1325-1335.	1.8	141
97	Screening Combinatorial Libraries by Mass Spectrometry. 2. Identification of Optimal Substrates of Protein Tyrosine Phosphatase SHP-1. <i>Biochemistry</i> , 2002, 41, 6202-6210.	2.5	37
98	High-Resolution Fourier Transform Ion Cyclotron Resonance Mass Spectrometry of Humic and Fulvic Acids: Improvements and Comparisons. <i>Analytical Chemistry</i> , 2002, 74, 413-419.	6.5	212
99	The application of electrospray ionization mass spectrometry (ESI MS) to the structural characterization of natural organic matter. <i>Organic Geochemistry</i> , 2002, 33, 171-180.	1.8	171
100	FT-ICR studies of polypyrazolyl-1-yl borates of europium(II) adducts. <i>Journal of Alloys and Compounds</i> , 2001, 323-324, 147-149.	5.5	5
101	Assignment of Gas-Phase Dipeptide Amide Hydrogen Exchange Rate Constants by Site-Specific Substitution: GlyGly. <i>Journal of Physical Chemistry B</i> , 2001, 105, 2244-2249.	2.6	21
102	Gas-phase hydrogen/deuterium exchange of positively charged mononucleotides by use of Fourier-transform ion cyclotron resonance mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 268-277.	2.8	48
103	Gas phase RNA and DNA ions 2. Conformational dependence of the gas-phase H/D exchange of nucleotide-5'-monophosphates. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 780-785.	2.8	31
104	Screening combinatorial libraries for optimal enzyme substrates by mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 1166-1171.	1.5	15
105	Compositional Analysis for Identification of Arson Accelerants by Electron Ionization Fourier Transform Ion Cyclotron Resonance High-Resolution Mass Spectrometry. <i>Journal of Forensic Sciences</i> , 2001, 46, 268-279.	1.6	21
106	<title>Correlation between solution and gas-phase protein conformation: H/D exchange, IRMPD, and ESI FT-ICR MS</title>. , 2000, , .		1
107	Comparison and interconversion of the two most common frequency-to-mass calibration functions for Fourier transform ion cyclotron resonance mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2000, 195-196, 591-598.	1.5	175
108	Competitive binding to the oligopeptide binding protein, OppA: In-trap cleanup in an fourier transform ion cyclotron resonance mass spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2000, 11, 1023-1026.	2.8	13



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109	Complete Compositional Monitoring of the Weathering of Transportation Fuels Based on Elemental Compositions from Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Environmental Science & Technology, 2000, 34, 1671-1678.	10.0	30
110	Determination of Relative Ordering of Activation Energies for Gas-Phase Ion Unimolecular Dissociation by Infrared Radiation for Gaseous Multiphoton Energy Transfer. Journal of the American Chemical Society, 2000, 122, 7768-7775.	13.7	37
111	Isotopic Amplification, H/D Exchange, and Other Mass Spectrometric Strategies for Characterization of Biomacromolecular Topology and Binding Sites. , 2000, , 31-52.		2
112	Gas-phase bovine ubiquitin cation conformations resolved by gas-phase hydrogen/deuterium exchange rate and extent. International Journal of Mass Spectrometry, 1999, 185-187, 565-575.	1.5	126
113	Gas-phase memory of solution-phase protein conformation: H/D exchange and Fourier transform ion cyclotron resonance mass spectrometry of the N-terminal domain of cardiac troponin C. International Journal of Mass Spectrometry, 1999, 192, 319-325.	1.5	45
114	Characterization of a single crystal cubic Prussian blue Co <sub>8</sub> (tacn) <sub>8</sub> (CN) <sub>12</sub> cluster by ion trap and Fourier transform ion cyclotron resonance mass spectrometry with microelectrospray ionization. Journal of the American Society for Mass Spectrometry, 1999, 10, 352-354.	2.8	5
115	Self-chemical ionization of diethylzinc. , 1999, 13, 1622-1625.		2
116	Gas phase activation energy for unimolecular dissociation of biomolecular ions determined by Focused RAdiation for Gaseous Multiphoton ENergy Transfer (FRAGMENT). , 1999, 13, 1639-1642.		40
117	Jet Fuel Chemical Composition, Weathering, and Identification as a Contaminant at a Remediation Site, Determined by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Analytical Chemistry, 1999, 71, 5171-5176.	6.5	35
118	Gas-Phase Hydrogen/Deuterium Exchange Reactions of Fulvic Acids: An Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectral Study. Analytical Chemistry, 1999, 71, 4719-4726.	6.5	54
119	High-field fourier transform ion cyclotron resonance mass spectrometry for simultaneous trapping and gas-phase hydrogen/deuterium exchange of peptide ions. Journal of the American Society for Mass Spectrometry, 1998, 9, 1012-1019.	2.8	57
120	Characterization of an ambident electrophile: the gas phase reactivity of the methoxymethyl cation. International Journal of Mass Spectrometry and Ion Processes, 1998, 175, 107-122.	1.8	18
121	Synthesis of Highly Charged Organometallic Dendrimers and Their Characterization by Electrospray Mass Spectrometry and Single-Crystal X-ray Diffraction. Journal of the American Chemical Society, 1998, 120, 12207-12215.	13.7	64
122	Gas-Phase RNA and DNA Ions. 1. H/D Exchange of the [M - H] <sup>-</sup> -Anions of Nucleoside 5'-Monophosphates (GMP, dGMP, AMP, dAMP, CMP, dCMP, UMP, dTMP), Ribose 5-Monophosphate, and 2-Deoxyribose 5-Monophosphate with D <sub>2</sub> O and D <sub>2</sub> S. Journal of the American Chemical Society, 1998, 120, 10187-10193.	13.7	59
123	The methoxymethyl cation cleaves peptide bonds in the gas phase. Chemical Communications, 1997, , 1409-1410.	4.1	18
124	Gas Phase Reactions of Cysteine with Charged Electrophiles: Regioselectivities of the Dimethylchlorinium Ion and the Methoxymethyl Cation. 1. Journal of Organic Chemistry, 1997, 62, 6112-6120.	3.2	28
125	Gas Phase Reactions of the Cyclic Ethylenehalonium Ions (CH <sub>2</sub> ) <sub>2</sub> X <sup>+</sup> (X = Cl, Br) with Glycine. 1. Journal of Organic Chemistry, 1996, 61, 2374-2382.	3.2	15
126	Gas-phase Reactions of Glycine, Alanine, Valine and their N-Methyl Derivatives with the Nitrosonium Ion, NO <sup>+</sup> . , 1996, 31, 1086-1092.		15



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127	Gas-phase methylation of the 2-hydroxypyridine/2-pyridone system by the dimethylchlorinium ion. European Journal of Mass Spectrometry, 1995, 1, 457.	0.7	11
128	Concerning the Regioselectivity of Gas Phase Reactions of Glycine with Electrophiles. The Cases of the Dimethylchlorinium Ion and the Methoxymethyl Cation. Journal of Organic Chemistry, 1995, 60, 1990-1998.	3.2	29
129	Citrate is a major component of snake venoms. Toxicon, 1992, 30, 461-464.	1.6	32
130	Studies of the structure of humic substances by electrospray ionization coupled to a quadrupole-time of flight (QQ-TOF) mass spectrometer. , 0, , 95-108.		4
131	Differential expression of histone post-translational modifications in acute myeloid and chronic lymphocytic leukemia determined by high-pressure liquid chromatography and mass spectrometry. Journal of the American Society for Mass Spectrometry, 0, , .	2.8	0