

Michael A Freitas

List of Publications by Year in descending order

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131
papers

5,459
citations

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7381
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| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Histone H3-K56 Acetylation Is Catalyzed by Histone Chaperone-Dependent Complexes. <i>Molecular Cell</i> , 2007, 25, 703-712. | 4.5 | 268 |
| 2 | Identification of novel histone post-translational modifications by peptide mass fingerprinting. <i>Chromosoma</i> , 2003, 112, 77-86. | 1.0 | 244 |
| 3 | 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. | 3.2 | 212 |
| 4 | H1 histones: current perspectives and challenges. <i>Nucleic Acids Research</i> , 2013, 41, 9593-9609. | 6.5 | 188 |
| 5 | 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. | 0.7 | 175 |
| 6 | 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. | 0.9 | 171 |
| 7 | MassMatrix: A database search program for rapid characterization of proteins and peptides from tandem mass spectrometry data. <i>Proteomics</i> , 2009, 9, 1548-1555. | 1.3 | 167 |
| 8 | Histone H4 Lysine 91 Acetylation. <i>Molecular Cell</i> , 2005, 18, 123-130. | 4.5 | 155 |
| 9 | Age-related changes in mesenchymal stem cells derived from rhesus macaque bone marrow. <i>Aging Cell</i> , 2011, 10, 66-79. | 3.0 | 142 |
| 10 | 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. | 0.9 | 141 |
| 11 | A mass accuracy sensitive probability based scoring algorithm for database searching of tandem mass spectrometry data. <i>BMC Bioinformatics</i> , 2007, 8, 133. | 1.2 | 127 |
| 12 | Gas-phase bovine ubiquitin cation conformations resolved by gas-phase hydrogen/deuterium exchange rate and extent. <i>International Journal of Mass Spectrometry</i> , 1999, 185-187, 565-575. | 0.7 | 126 |
| 13 | Application of mass spectrometry to the identification and quantification of histone post-translational modifications. <i>Journal of Cellular Biochemistry</i> , 2004, 92, 691-700. | 1.2 | 125 |
| 14 | 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. | 1.8 | 123 |
| 15 | Tetraspanin CD37 Directly Mediates Transduction of Survival and Apoptotic Signals. <i>Cancer Cell</i> , 2012, 21, 694-708. | 7.7 | 122 |
| 16 | In vivo NCL targeting affects breast cancer aggressiveness through miRNA regulation. <i>Journal of Experimental Medicine</i> , 2013, 210, 951-968. | 4.2 | 121 |
| 17 | Identification of Histone Demethylases in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 14262-14271. | 1.6 | 96 |
| 18 | Database Search Algorithm for Identification of Intact Cross-Links in Proteins and Peptides Using Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 3384-3393. | 1.8 | 72 |

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| 19 | Proteomic Analysis Reveals New Cardiac-Specific Dystrophin-Associated Proteins. PLoS ONE, 2012, 7, e43515. | 1.1 | 72 |
| 20 | 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. | 0.4 | 72 |
| 21 | The long non-coding RNA HOXB-AS3 regulates ribosomal RNA transcription in NPM1-mutated acute myeloid leukemia. Nature Communications, 2019, 10, 5351. | 5.8 | 71 |
| 22 | Proteomic characterization of circulating extracellular vesicles identifies novel serum myeloma associated markers. Journal of Proteomics, 2016, 136, 89-98. | 1.2 | 68 |
| 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. | 1.6 | 68 |
| 24 | 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. | 6.6 | 64 |
| 25 | 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. | 1.3 | 64 |
| 26 | Gas-Phase RNA and DNA Ions. 1. H/D Exchange of the [M + H]-Anions of Nucleoside 5'-Monophosphates (GMP, dGMP, AMP, dAMP, CMP, dCMP, UMP, dTMP), Ribose 5-Monophosphate, and 2-Deoxyribose 5-Monophosphate with D2O and D2S. Journal of the American Chemical Society, 1998, 120, 10187-10193. | 6.6 | 59 |
| 27 | 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, 2004, 15, 77-86. | 1.2 | 59 |
| 28 | 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. | 3.3 | 58 |
| 29 | 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. | 1.2 | 57 |
| 30 | Characterization of glomerular diseases using proteomic analysis of laser capture microdissected glomeruli. Modern Pathology, 2012, 25, 709-721. | 2.9 | 57 |
| 31 | 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. | 3.2 | 54 |
| 32 | Peptide-Based Inhibition of NF- κ B Rescues Diaphragm Muscle Contractile Dysfunction in a Murine Model of Duchenne Muscular Dystrophy. Molecular Medicine, 2011, 17, 508-515. | 1.9 | 51 |
| 33 | The impact of cruciferous vegetable isothiocyanates on histone acetylation and histone phosphorylation in bladder cancer. Journal of Proteomics, 2017, 156, 94-103. | 1.2 | 49 |
| 34 | The Novel Deacetylase Inhibitor AR-42 Demonstrates Pre-Clinical Activity in B-Cell Malignancies In Vitro and In Vivo. PLoS ONE, 2010, 5, e10941. | 1.1 | 49 |
| 35 | Gas-phase hydrogen/deuterium exchange of positively charged mononucleotides by use of Fourier-transform ion cyclotron resonance mass spectrometry. Journal of the American Society for Mass Spectrometry, 2001, 12, 268-277. | 1.2 | 48 |
| 36 | Apigenin induces DNA damage through the PKC δ -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. | 2.0 | 46 |

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| 37 | 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. <i>International Journal of Mass Spectrometry</i> , 1999, 192, 319-325. | 0.7 | 45 |
| 38 | 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. | 1.2 | 44 |
| 39 | Monte Carlo Simulation-Based Algorithms for Analysis of Shotgun Proteomic Data. <i>Journal of Proteome Research</i> , 2008, 7, 2605-2615. | 1.8 | 41 |
| 40 | 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 |
| 41 | Mass spectrometry-based strategies for characterization of histones and their post-translational modifications. <i>Expert Review of Proteomics</i> , 2007, 4, 211-225. | 1.3 | 38 |
| 42 | A quantitative proteomic workflow for characterization of frozen clinical biopsies: Laser capture microdissection coupled with label-free mass spectrometry. <i>Journal of Proteomics</i> , 2012, 77, 433-440. | 1.2 | 38 |
| 43 | Histone H1 Phosphorylation in Breast Cancer. <i>Journal of Proteome Research</i> , 2014, 13, 2453-2467. | 1.8 | 38 |
| 44 | Determination of Relative Ordering of Activation Energies for Gas-Phase Ion Unimolecular Dissociation by Infrared Radiation for Gaseous Multiphoton Energy Transfer. <i>Journal of the American Chemical Society</i> , 2000, 122, 7768-7775. | 6.6 | 37 |
| 45 | Screening Combinatorial Libraries by Mass Spectrometry. 2. Identification of Optimal Substrates of Protein Tyrosine Phosphatase SHP-1. <i>Biochemistry</i> , 2002, 41, 6202-6210. | 1.2 | 37 |
| 46 | 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. | 1.2 | 37 |
| 47 | Identification of multiple roles for histone acetyltransferase 1 in replication-coupled chromatin assembly. <i>Nucleic Acids Research</i> , 2017, 45, 9319-9335. | 6.5 | 37 |
| 48 | Jet Fuel Chemical Composition, Weathering, and Identification as a Contaminant at a Remediation Site, Determined by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 1999, 71, 5171-5176. | 3.2 | 35 |
| 49 | Alterations of Histone H1 Phosphorylation During Bladder Carcinogenesis. <i>Journal of Proteome Research</i> , 2013, 12, 3317-3326. | 1.8 | 34 |
| 50 | Discovery of Histone Modification Crosstalk Networks by Stable Isotope Labeling of Amino Acids in Cell Culture Mass Spectrometry (SILAC MS). <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2048-2059. | 2.5 | 33 |
| 51 | Citrate is a major component of snake venoms. <i>Toxicon</i> , 1992, 30, 461-464. | 0.8 | 32 |
| 52 | Characterization of Multiple Myeloma Vesicles by Label-Free Relative Quantitation. <i>Proteomics</i> , 2013, 13, n/a-n/a. | 1.3 | 32 |
| 53 | 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. | 1.2 | 31 |
| 54 | Middle-Down Characterization of the Cell Cycle Dependence of Histone H4 Posttranslational Modifications and Proteoforms. <i>Proteomics</i> , 2018, 18, e1700442. | 1.3 | 31 |

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| 55 | Complete Compositional Monitoring of the Weathering of Transportation Fuels Based on Elemental Compositions from Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Environmental Science & Technology</i> , 2000, 34, 1671-1678. | 4.6 | 30 |
| 56 | Concerning the Regioselectivity of Gas Phase Reactions of Glycine with Electrophiles. The Cases of the Dimethylchlorinium Ion and the Methoxymethyl Cation. <i>Journal of Organic Chemistry</i> , 1995, 60, 1990-1998. | 1.7 | 29 |
| 57 | 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. | 0.7 | 29 |
| 58 | 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. | 1.2 | 29 |
| 59 | Quantitative Mass Spectrometry Reveals that Intact Histone H1 Phosphorylations are Variant Specific and Exhibit Single Molecule Hierarchical Dependence. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 818-833. | 2.5 | 29 |
| 60 | Gas Phase Reactions of Cysteine with Charged Electrophiles: Regioselectivities of the Dimethylchlorinium Ion and the Methoxymethyl Cation. <i>Journal of Organic Chemistry</i> , 1997, 62, 6112-6120. | 1.7 | 28 |
| 61 | The chromatin scaffold protein SAFB1 localizes SUMO-1 to the promoters of ribosomal protein genes to facilitate transcription initiation and splicing. <i>Nucleic Acids Research</i> , 2015, 43, 3605-3613. | 6.5 | 27 |
| 62 | Sites of Acetylation on Newly Synthesized Histone H4 Are Required for Chromatin Assembly and DNA Damage Response Signaling. <i>Molecular and Cellular Biology</i> , 2013, 33, 3286-3298. | 1.1 | 26 |
| 63 | Increasing the complexity of chromatin: functionally distinct roles for replication-dependent histone H2A isoforms in cell proliferation and carcinogenesis. <i>Nucleic Acids Research</i> , 2013, 41, 9284-9295. | 6.5 | 25 |
| 64 | Histone acetyltransferase 1 is required for DNA replication fork function and stability. <i>Journal of Biological Chemistry</i> , 2020, 295, 8363-8373. | 1.6 | 23 |
| 65 | Quantitative profiling of histone post-translational modifications by stable isotope labeling. <i>Methods</i> , 2007, 41, 312-319. | 1.9 | 22 |
| 66 | Validation of an LC-MS based approach for profiling histones in chronic lymphocytic leukemia. <i>Proteomics</i> , 2009, 9, 1197-1206. | 1.3 | 22 |
| 67 | 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. | 1.2 | 21 |
| 68 | 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. | 0.9 | 21 |
| 69 | 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. | 1.8 | 20 |
| 70 | Automated diagnosis of LC-MS/MS performance. <i>Bioinformatics</i> , 2009, 25, 1341-1343. | 1.8 | 20 |
| 71 | A multi-model statistical approach for proteomic spectral count quantitation. <i>Journal of Proteomics</i> , 2016, 144, 23-32. | 1.2 | 20 |
| 72 | Multiple Imputation Approaches Applied to the Missing Value Problem in Bottom-Up Proteomics. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9650. | 1.8 | 20 |

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|----|--|-----|-----------|
| 73 | 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. | 1.1 | 19 |
| 74 | A Dynamic Noise Level Algorithm for Spectral Screening of Peptide MS/MS Spectra. <i>BMC Bioinformatics</i> , 2010, 11, 436. | 1.2 | 19 |
| 75 | Unambiguous determination of isobaric histone modifications by reversed-phase retention time and high-mass accuracy. <i>Analytical Biochemistry</i> , 2010, 396, 13-22. | 1.1 | 19 |
| 76 | Methylation of the PTPRO gene in human hepatocellular carcinoma and identification of VCP as its substrate. <i>Journal of Cellular Biochemistry</i> , 2013, 114, 1810-1818. | 1.2 | 19 |
| 77 | The methoxymethyl cation cleaves peptide bonds in the gas phase. <i>Chemical Communications</i> , 1997, , 1409-1410. | 2.2 | 18 |
| 78 | Characterization of an ambident electrophile: the gas phase reactivity of the methoxymethyl cation. <i>International Journal of Mass Spectrometry and Ion Processes</i> , 1998, 175, 107-122. | 1.9 | 18 |
| 79 | Proteomic profiling identifies specific histone species associated with leukemic and cancer cells. <i>Clinical Proteomics</i> , 2015, 12, 22. | 1.1 | 18 |
| 80 | Biological aging alters circadian mechanisms in murine adipose tissue depots. <i>Age</i> , 2013, 35, 533-547. | 3.0 | 17 |
| 81 | The proinflammatory protein HMGB1 is a substrate of transglutaminase-2 and forms high-molecular weight complexes with autoantigens. <i>Journal of Biological Chemistry</i> , 2018, 293, 8394-8409. | 1.6 | 17 |
| 82 | Gas Phase Reactions of the Cyclic Ethylenehalonium Ions (CH ₂) ₂ X ⁺ (X = Cl, Br) with Glycine ¹ . <i>Journal of Organic Chemistry</i> , 1996, 61, 2374-2382. | 1.7 | 15 |
| 83 | Gas-phase Reactions of Glycine, Alanine, Valine and their N-Methyl Derivatives with the Nitrosonium Ion, NO ⁺ . , 1996, 31, 1086-1092. | | 15 |
| 84 | Screening combinatorial libraries for optimal enzyme substrates by mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 1166-1171. | 0.7 | 15 |
| 85 | The non-canonical hydroxylase structure of YfcM reveals a metal ion-coordination motif required for EF-P hydroxylation. <i>Nucleic Acids Research</i> , 2014, 42, 12295-12305. | 6.5 | 15 |
| 86 | A Cloud-based Dynamic Workflow for Mass Spectrometry Data Analysis. , 2011, , . | | 14 |
| 87 | Specificity Profiling of Dual Specificity Phosphatase Vaccinia VH1-related (VHR) Reveals Two Distinct Substrate Binding Modes*. <i>Journal of Biological Chemistry</i> , 2013, 288, 6498-6510. | 1.6 | 14 |
| 88 | Epigenetic regulation of nuclear lamina-associated heterochromatin by HAT1 and the acetylation of newly synthesized histones. <i>Nucleic Acids Research</i> , 2021, 49, 12136-12151. | 6.5 | 14 |
| 89 | Competitive binding to the oligopeptide binding protein, OppA: In-trap cleanup in a fourier transform ion cyclotron resonance mass spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2000, 11, 1023-1026. | 1.2 | 13 |
| 90 | 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. | 1.2 | 13 |

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| 91 | A hierarchical MS ² /MS ³ database search algorithm for automated analysis of phosphopeptide tandem mass spectra. <i>Proteomics</i> , 2009, 9, 1763-1770. | 1.3 | 13 |
| 92 | Assaying pharmacodynamic endpoints with targeted therapy: Flavopiridol and 17AAG induced dephosphorylation of histone H1.5 in acute myeloid leukemia. <i>Proteomics</i> , 2010, 10, 4281-4292. | 1.3 | 13 |
| 93 | Spinal Muscular Atrophy Biomarker Measurements from Blood Samples in a Clinical Trial of Valproic Acid in Ambulatory Adults. <i>Journal of Neuromuscular Diseases</i> , 2015, 2, 119-130. | 1.1 | 13 |
| 94 | 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. | 0.7 | 12 |
| 95 | Isolation and analysis of linker histones across cellular compartments. <i>Journal of Proteomics</i> , 2013, 91, 595-604. | 1.2 | 12 |
| 96 | Trauma induced heterotopic ossification patient serum alters mitogen activated protein kinase signaling in adipose stem cells. <i>Journal of Cellular Physiology</i> , 2018, 233, 7035-7044. | 2.0 | 12 |
| 97 | Detection of single peptide with only one amino acid modification via electronic fingerprinting using reengineered durable channel of Phi29 DNA packaging motor. <i>Biomaterials</i> , 2021, 276, 121022. | 5.7 | 12 |
| 98 | Gas-phase methylation of the 2-hydroxypyridine/2-pyridone system by the dimethylchlorinium ion. <i>European Journal of Mass Spectrometry</i> , 1995, 1, 457. | 0.7 | 11 |
| 99 | High sensitivity TFA-free LC-MS for profiling histones. <i>Proteomics</i> , 2011, 11, 3326-3334. | 1.3 | 10 |
| 100 | The potential diagnostic power of extracellular vesicle analysis for multiple myeloma. <i>Expert Review of Molecular Diagnostics</i> , 2016, 16, 277-284. | 1.5 | 10 |
| 101 | Enrichment and characterization of histones by two-dimensional hydroxyapatite/reversed-phase liquid chromatography-mass spectrometry. <i>Analytical Biochemistry</i> , 2009, 388, 47-55. | 1.1 | 9 |
| 102 | Identification of replication-dependent and replication-independent linker histone complexes: Tpr specifically promotes replication-dependent linker histone stability. <i>BMC Biochemistry</i> , 2016, 17, 18. | 4.4 | 9 |
| 103 | Fractionation of DNA and protein from individual latent fingerprints for forensic analysis. <i>Forensic Science International: Genetics</i> , 2021, 50, 102405. | 1.6 | 9 |
| 104 | Proteomic Signatures of Thymomas. <i>PLoS ONE</i> , 2016, 11, e0166494. | 1.1 | 9 |
| 105 | The functional impact of BRCA1 BRCT domain variants using multiplexed DNA double-strand break repair assays. <i>American Journal of Human Genetics</i> , 2022, 109, 618-630. | 2.6 | 8 |
| 106 | Tag-Count Analysis of Large-Scale Proteomic Data. <i>Journal of Proteome Research</i> , 2016, 15, 4742-4746. | 1.8 | 7 |
| 107 | Characterization of a single crystal cubic Prussian blue Co ₈ (tacn) ₈ (CN) ₁₂ cluster by ion trap and Fourier transform ion cyclotron resonance mass spectrometry with microelectrospray ionization. <i>Journal of the American Society for Mass Spectrometry</i> , 1999, 10, 352-354. | 1.2 | 5 |
| 108 | FT-ICR studies of polypyrazolyl-1-yl borates of europium(II) adducts. <i>Journal of Alloys and Compounds</i> , 2001, 323-324, 147-149. | 2.8 | 5 |

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| 109 | Using ontology-based methods for implementing role-based access control in cooperative systems. , 2012, , . | | 5 |
| 110 | Simultaneous metabolic labeling of cells with multiple amino acids: Localization and dynamics of histone acetylation and methylation. Proteomics - Clinical Applications, 2007, 1, 130-142. | 0.8 | 4 |
| 111 | SILAC Peptide Ratio Calculator: A Tool for SILAC Quantitation of Peptides and Post-Translational Modifications. Journal of Proteome Research, 2014, 13, 506-516. | 1.8 | 4 |
| 112 | Tagging enhances histochemical and biochemical detection of Ran Binding Protein 9 in vivo and reveals its interaction with Nucleolin. Scientific Reports, 2020, 10, 7138. | 1.6 | 4 |
| 113 | An algorithm for random match probability calculation from peptide sequences. Forensic Science International: Genetics, 2020, 47, 102295. | 1.6 | 4 |
| 114 | Optimization of proteomics sample preparation for forensic analysis of skin samples. Journal of Proteomics, 2021, 249, 104360. | 1.2 | 4 |
| 115 | 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 |
| 116 | Self-chemical ionization of diethylzinc. , 1999, 13, 1622-1625. | | 2 |
| 117 | Isolation of Proteins on Nascent Chromatin and Characterization by Quantitative Mass Spectrometry. Methods in Molecular Biology, 2019, 1983, 17-27. | 0.4 | 2 |
| 118 | Isotopic Amplification, H/D Exchange, and Other Mass Spectrometric Strategies for Characterization of Biomacromolecular Topology and Binding Sites. , 2000, , 31-52. | | 2 |
| 119 | Techniques for estimating genetically variable peptides and semi-continuous likelihoods from massively parallel sequencing data. Forensic Science International: Genetics, 2022, 59, 102719. | 1.6 | 2 |
| 120 | <title>Correlation between solution and gas-phase protein conformation: H/D exchange, IRMPD, and ESI FT-ICR MS</title>. , 2000, , . | | 1 |
| 121 | Using Semantic Web Technologies for RBAC in Project-Oriented Environments. , 2012, , . | | 1 |
| 122 | 8: Epigenetics and microRNA as a unifying mechanism in severe preeclampsia. American Journal of Obstetrics and Gynecology, 2014, 210, S5. | 0.7 | 1 |
| 123 | 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. | 1.2 | 1 |
| 124 | TIMSCONVERT: a workflow to convert trapped ion mobility data to open data formats. Bioinformatics, 2022, 38, 4046-4047. | 1.8 | 1 |
| 125 | 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, , . | 1.2 | 0 |
| 126 | Abstract 1351: Analysis of the in vivo tumor suppressive potential of PTPROt (truncated protein) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 6 | | |

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|-----|---|-----|-----------|
| 127 | In vivo NCL targeting affects breast cancer aggressiveness through miRNA regulation. Journal of Cell Biology, 2013, 201, i4-i4. | 2.3 | 0 |
| 128 | Abstract 1122: In vivo NCL-targeting affects breast cancer aggressiveness through miRNA regulation., 2013, , . | | 0 |
| 129 | Abstract 3335: Characterizing the MAXH28Rsecretome in endometrial cancer. , 2018, , . | | 0 |
| 130 | Abstract 1285: Deep mutagenesis analysis on BRCA1 variants in high throughput DNA repair assays. , 2018, , . | | 0 |
| 131 | Abstract 1367: BRCA1 and BARD1 protein interactions that are required for DNA repair function. , 2018, , . | | 0 |