## Ron Bonner

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Targeted Data Extraction of the MS/MS Spectra Generated by Data-independent Acquisition: A New Concept for Consistent and Accurate Proteome Analysis. Molecular and Cellular Proteomics, 2012, 11, O111.016717.	3.8	2,285
2	The determination of protein, oligonucleotide and peptide molecular weights by ion-spray mass spectrometry. Rapid Communications in Mass Spectrometry, 1988, 2, 249-256.	1.5	584
3	Automated Identification and Quantification of Glycerophospholipid Molecular Species by Multiple Precursor Ion Scanning. Analytical Chemistry, 2006, 78, 6202-6214.	6.5	379
4	Mapping differential interactomes by affinity purification coupled with data-independent mass spectrometry acquisition. Nature Methods, 2013, 10, 1239-1245.	19.0	277
5	Application of Wavelet Transforms to Experimental Spectra:Â Smoothing, Denoising, and Data Set Compression. Analytical Chemistry, 1997, 69, 78-90.	6.5	229
6	Selected reaction monitoring mass spectrometry reveals the dynamics of signaling through the GRB2 adaptor. Nature Biotechnology, 2011, 29, 653-658.	17.5	209
7	Dimensionality Reduction and Visualization in Principal Component Analysis. Analytical Chemistry, 2008, 80, 4933-4944.	6.5	170
8	Radioâ€frequency mass selective excitation and resonant ejection of ions in a threeâ€dimensional quadrupole ion trap. Journal of Vacuum Science and Technology, 1980, 17, 829-835.	1.9	118
9	Exact mass measurement of product ions for the structural elucidation of drug metabolites with a tandem quadrupole orthogonal-acceleration time-of-flight mass spectrometer. Journal of the American Society for Mass Spectrometry, 1999, 10, 1305-1314.	2.8	86
10	The cylindrical ion trap. Part I. General introduction. International Journal of Mass Spectrometry and Ion Physics, 1977, 24, 255-269.	1.3	75
11	Instrumental and experimental effects in LC–MS-based metabolomics. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2008, 871, 227-235.	2.3	60
12	SWATH data independent acquisition mass spectrometry for metabolomics. TrAC - Trends in Analytical Chemistry, 2019, 120, 115278.	11.4	58
13	Label-free quantitative proteomics trends for protein–protein interactions. Journal of Proteomics, 2013, 81, 91-101.	2.4	55
14	Effect of charge exchange reactions on the motion of ions in three-dimensional quadrupole electric fields. International Journal of Mass Spectrometry and Ion Physics, 1976, 22, 17-34.	1.3	45
15	Methodological considerations in the development of HPLC-MS methods for the analysis of rodent plasma for metabonomic studies. Molecular BioSystems, 2009, 6, 108-120.	2.9	45
16	Ion-molecule reaction studies with a quadrupole ion storage trap. International Journal of Mass Spectrometry and Ion Physics, 1972, 10, 197-203.	1.3	41
17	SWATH acquisition mode for drug metabolism and metabolomics investigations. Bioanalysis, 2016, 8, 1735-1750.	1.5	39
18	SWATH-MS for metabolomics and lipidomics: critical aspects of qualitative and quantitative analysis. Metabolomics, 2020, 16, 71.	3.0	36

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19	Comprehensive Analytical Strategy for Biomarker Identification based on Liquid Chromatography Coupled to Mass Spectrometry and New Candidate Confirmation Tools. Analytical Chemistry, 2009, 81, 7677-7694.	6.5	31
20	Metabolomic spectral libraries for data-independent SWATH liquid chromatography mass spectrometry acquisition. Analytical and Bioanalytical Chemistry, 2018, 410, 1873-1884.	3.7	30
21	Derivations of the field equations and stability parameters for three operating modes of the three-dimensional quadrupole. International Journal of Mass Spectrometry and Ion Physics, 1977, 23, 249-257.	1.3	28
22	The effects of charge exchange collisions on the motion of ions in three-dimensional quadrupole electric fields Part II. Program improvements and fundamental results. International Journal of Mass Spectrometry and Ion Physics, 1977, 25, 411-431.	1.3	27
23	Complexity among constituents of the HLA-B*1501 peptide motif. Immunogenetics, 1998, 48, 89-97.	2.4	27
24	The quadrupole ion store (QUISTOR) part VIII. The theoretical estimation of ion kinetic energies: A comparative survey of the field. International Journal of Mass Spectrometry and Ion Physics, 1980, 34, 17-36.	1.3	23
25	SWATH data independent acquisition mass spectrometry for screening of xenobiotics in biological fluids: Opportunities and challenges for data processing. Talanta, 2020, 211, 120747.	5.5	22
26	Adduct annotation in liquid chromatography/high-resolution mass spectrometry to enhance compound identification. Analytical and Bioanalytical Chemistry, 2021, 413, 503-517.	3.7	17
27	High-performance digital timing system. Analytical Chemistry, 1980, 52, 1923-1928.	6.5	16
28	Effects of charge-exchange reactions on the motion of ions in three-dimensional quadrupole electric fields. part III. a two-ion model. International Journal of Mass Spectrometry and Ion Physics, 1980, 33, 139-158.	1.3	13
29	The characterization of proteins and peptides by automated methods. Rapid Communications in Mass Spectrometry, 1995, 9, 1067-1076.	1.5	13
30	Hybrid SWATH/MS and HR-SRM/MS acquisition for phospholipidomics using QUAL/QUANT data processing. Analytical and Bioanalytical Chemistry, 2019, 411, 5681-5690.	3.7	13
31	Development of a highly automated and multiplexed targeted proteome pipeline and assay for 112 rat brain synaptic proteins. Proteomics, 2015, 15, 1202-1214.	2.2	12
32	Improved metabolite characterization by liquid chromatography – Tandem mass spectrometry through electron impact type fragments from adduct ions. Analytica Chimica Acta, 2021, 1150, 338207.	5.4	10
33	Characterization of Protein Digests Using Novel Mixed-mode Scanning with a Single Quadrupole Instrument. Rapid Communications in Mass Spectrometry, 1997, 11, 325-329.	1.5	9
34	Utility of multivariate analysis in support of <i>in vitro</i> metabolite identification studies: retrospective analysis using the antidepressant drug nefazodone. Xenobiotica, 2010, 40, 262-274.	1.1	9
35	Metabolomics data complemented drug use information in epidemiological databases: pilot study of potential kidney donors. Journal of Clinical Epidemiology, 2021, 135, 10-16.	5.0	9
36	Error-tolerant protein database searching using peptide product-ion spectra. Rapid Communications in Mass Spectrometry, 1995, 9, 1077-1080.	1.5	8

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37	Annotation of complex mass spectra by multi-layered analysis. Analytica Chimica Acta, 2022, 1193, 339317.	5.4	7
38	Calculation of the phase-space parameters for the study of quadrupole devices. International Journal of Mass Spectrometry and Ion Physics, 1979, 30, 365-371.	1.3	6
39	Characterization of phospho-proteins in bovine and buffalo caseins using atmospheric pressure ionization mass spectrometry. Organic Mass Spectrometry, 1992, 27, 211-214.	1.3	5
40	Environmental analysis with a triple quadrupole. International Journal of Mass Spectrometry and Ion Physics, 1983, 48, 311-314.	1.3	4
41	Untargeted â€~SWATH' mass spectrometry-based metabolomics for studying chronic and intermittent exposure to xenobiotics in cohort studies. Food and Chemical Toxicology, 2022, 165, 113188.	3.6	3