

# Michael R Shortreed

## List of Publications by Year in descending order

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92  
papers

4,691  
citations

117625

34  
h-index

106344

65  
g-index

98  
all docs

98  
docs citations

98  
times ranked

5353  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fluorescent Fiber-Optic Calcium Sensor for Physiological Measurements. <i>Analytical Chemistry</i> , 1996, 68, 1414-1418.	6.5	605
2	Sirt3 Promotes the Urea Cycle and Fatty Acid Oxidation during Dietary Restriction. <i>Molecular Cell</i> , 2011, 41, 139-149.	9.7	344
3	Spectroscopic Evidence for Excitonic Localization in Fractal Antenna Supermolecules. <i>Physical Review Letters</i> , 1997, 78, 1239-1242.	7.8	295
4	Directed Energy Transfer Funnels in Dendrimeric Antenna Supermolecules. <i>Journal of Physical Chemistry B</i> , 1997, 101, 6318-6322.	2.6	279
5	Enhanced Global Post-translational Modification Discovery with MetaMorpheus. <i>Journal of Proteome Research</i> , 2018, 17, 1844-1851.	3.7	206
6	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361.	2.2	147
7	Miniature Sodium-Selective Ion-Exchange Optode with Fluorescent pH Chromoionophores and Tunable Dynamic Range. <i>Analytical Chemistry</i> , 1996, 68, 2656-2662.	6.5	129
8	Real-Time Dynamics of Single-DNA Molecules Undergoing Adsorption and Desorption at Liquid-Solid Interfaces. <i>Analytical Chemistry</i> , 2001, 73, 1091-1099.	6.5	118
9	Discovery and Mass Spectrometric Analysis of Novel Splice-junction Peptides Using RNA-Seq. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2341-2353.	3.8	115
10	O-Pair Search with MetaMorpheus for O-glycopeptide characterization. <i>Nature Methods</i> , 2020, 17, 1133-1138.	19.0	98
11	Proteogenomics: Integrating Next-Generation Sequencing and Mass Spectrometry to Characterize Human Proteomic Variation. <i>Annual Review of Analytical Chemistry</i> , 2016, 9, 521-545.	5.4	91
12	Analysis of Cell Surface Carbohydrate Expression Patterns in Normal and Tumorigenic Human Breast Cell Lines Using Lectin Arrays. <i>Analytical Chemistry</i> , 2007, 79, 5698-5702.	6.5	88
13	High-Throughput Single-Molecule Spectroscopy in Free Solution. <i>Analytical Chemistry</i> , 2000, 72, 4640-4645.	6.5	81
14	Large-Scale Mass Spectrometric Detection of Variant Peptides Resulting from Nonsynonymous Nucleotide Differences. <i>Journal of Proteome Research</i> , 2014, 13, 228-240.	3.7	81
15	$\beta$ -Ketoisocaproate-induced hypersecretion of insulin by islets from diabetes-susceptible mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2005, 289, E218-E224.	3.5	78
16	High-Throughput Single-Molecule DNA Screening Based on Electrophoresis. <i>Analytical Chemistry</i> , 2000, 72, 2879-2885.	6.5	77
17	Global Post-Translational Modification Discovery. <i>Journal of Proteome Research</i> , 2017, 16, 1383-1390.	3.7	75
18	Using Galaxy-P to leverage RNA-Seq for the discovery of novel protein variations. <i>BMC Genomics</i> , 2014, 15, 703.	2.8	74

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19	Ultrafast Peptide Label-Free Quantification with FlashLFQ. <i>Journal of Proteome Research</i> , 2018, 17, 386-391.	3.7	74
20	Relative Quantification of Carboxylic Acid Metabolites by Liquid Chromatography-Mass Spectrometry Using Isotopic Variants of Choline. <i>Analytical Chemistry</i> , 2007, 79, 5143-5149.	6.5	71
21	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1783-1802.	2.8	67
22	Ionizable Isotopic Labeling Reagent for Relative Quantification of Amine Metabolites by Mass Spectrometry. <i>Analytical Chemistry</i> , 2006, 78, 6398-6403.	6.5	62
23	Carbon-on-Metal Films for Surface Plasmon Resonance Detection of DNA Arrays. <i>Journal of the American Chemical Society</i> , 2008, 130, 8611-8613.	13.7	60
24	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019, 16, 939-940.	19.0	55
25	Thermodynamically based DNA strand design. <i>Nucleic Acids Research</i> , 2005, 33, 4951-4964.	14.5	54
26	Development of a fluorescent optical potassium-selective ion sensor with ratiometric response for intracellular applications. <i>Sensors and Actuators B: Chemical</i> , 1997, 38, 8-12.	7.8	49
27	Specific Capture of Mammalian Cells by Cell Surface Receptor Binding to Ligand Immobilized on Gold Thin Films. <i>Journal of Proteome Research</i> , 2006, 5, 1580-1585.	3.7	46
28	Global Identification of Protein Post-translational Modifications in a Single-Pass Database Search. <i>Journal of Proteome Research</i> , 2015, 14, 4714-4720.	3.7	43
29	Elucidating Proteoform Families from Proteoform Intact-Mass and Lysine-Count Measurements. <i>Journal of Proteome Research</i> , 2016, 15, 1213-1221.	3.7	43
30	Proteoform Suite: Software for Constructing, Quantifying, and Visualizing Proteoform Families. <i>Journal of Proteome Research</i> , 2018, 17, 568-578.	3.7	40
31	Identification of MS-Cleavable and Noncleavable Chemically Cross-Linked Peptides with MetaMorpheus. <i>Journal of Proteome Research</i> , 2018, 17, 2370-2376.	3.7	40
32	In situ oligonucleotide synthesis on carbon materials: stable substrates for microarray fabrication. <i>Nucleic Acids Research</i> , 2007, 36, e7-e7.	14.5	39
33	Comment on "A subset of HLA-I peptides are not genomically templated: Evidence for cis- and trans-spliced peptide ligands". <i>Science Immunology</i> , 2019, 4, .	11.9	39
34	Utilization of Lipophilic Ionic Additives in Liquid Polymer Film Optodes for Selective Anion Activity Measurements. <i>Analytical Chemistry</i> , 1997, 69, 990-995.	6.5	38
35	A thermodynamic approach to designing structure-free combinatorial DNA word sets. <i>Nucleic Acids Research</i> , 2005, 33, 4965-4977.	14.5	36
36	Improved Protein Inference from Multiple Protease Bottom-Up Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2019, 18, 3429-3438.	3.7	36

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37	Parallel Single Nucleotide Polymorphism Genotyping by Surface Invasive Cleavage with Universal Detection. <i>Analytical Chemistry</i> , 2005, 77, 2400-2405.	6.5	35
38	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018, 17, 1321-1325.	3.7	35
39	Enhanced protein isoform characterization through long-read proteogenomics. <i>Genome Biology</i> , 2022, 23, 69.	8.8	33
40	Elucidating <i>Escherichia coli</i> Proteoform Families Using Intact-Mass Proteomics and a Global PTM Discovery Database. <i>Journal of Proteome Research</i> , 2017, 16, 4156-4165.	3.7	32
41	Global Identification of Post-Translationally Spliced Peptides with Neo-Fusion. <i>Journal of Proteome Research</i> , 2018, 18, 349-358.	3.7	32
42	Sequence-Specific Capture of Protein-DNA Complexes for Mass Spectrometric Protein Identification. <i>PLoS ONE</i> , 2011, 6, e26217.	2.5	30
43	Structure-Specific DNA Cleavage on Surfaces. <i>Journal of the American Chemical Society</i> , 2002, 124, 7924-7931.	13.7	29
44	Human Proteomic Variation Revealed by Combining RNA-Seq Proteogenomics and Global Post-Translational Modification (G-PTM) Search Strategy. <i>Journal of Proteome Research</i> , 2016, 15, 800-808.	3.7	29
45	Expanding Proteoform Identifications in Top-Down Proteomic Analyses by Constructing Proteoform Families. <i>Analytical Chemistry</i> , 2018, 90, 1325-1333.	6.5	27
46	Improving Proteoform Identifications in Complex Systems Through Integration of Bottom-Up and Top-Down Data. <i>Journal of Proteome Research</i> , 2020, 19, 3510-3517.	3.7	25
47	Spritz: A Proteogenomic Database Engine. <i>Journal of Proteome Research</i> , 2021, 20, 1826-1834.	3.7	24
48	Single-molecule immunoassay and DNA diagnosis. <i>Electrophoresis</i> , 2001, 22, 421-426.	2.4	23
49	Identification and Quantification of Murine Mitochondrial Proteoforms Using an Integrated Top-Down and Intact-Mass Strategy. <i>Journal of Proteome Research</i> , 2018, 17, 3526-3536.	3.7	23
50	Discovery of Chromatin-Associated Proteins via Sequence-Specific Capture and Mass Spectrometric Protein Identification in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2014, 13, 3810-3825.	3.7	21
51	Constructing Human Proteoform Families Using Intact-Mass and Top-Down Proteomics with a Multi-Protease Global Post-Translational Modification Discovery Database. <i>Journal of Proteome Research</i> , 2019, 18, 3671-3680.	3.7	21
52	Anion-selective liquid-polymer optodes with fluorescent pH chromoionophores, tunable dynamic range and diffusion enhanced lifetimes. <i>Sensors and Actuators B: Chemical</i> , 1996, 35, 217-221.	7.8	20
53	Surface Amplification of Invasive Cleavage Products. <i>Journal of the American Chemical Society</i> , 2004, 126, 3016-3017.	13.7	20
54	Compartmentalization of HP1 Proteins in Pluripotency Acquisition and Maintenance. <i>Stem Cell Reports</i> , 2018, 10, 627-641.	4.8	20

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55	Scoring Single-Nucleotide Polymorphisms at the Single-Molecule Level by Counting Individual DNA Cleavage Events on Surfaces. <i>Analytical Chemistry</i> , 2005, 77, 6594-6600.	6.5	19
56	Multiplexed Analysis of Cage and Cage Free Chicken Egg Fatty Acids Using Stable Isotope Labeling and Mass Spectrometry. <i>Molecules</i> , 2013, 18, 14977-14988.	3.8	17
57	Proteomics in non-human primates: utilizing RNA-Seq data to improve protein identification by mass spectrometry in vervet monkeys. <i>BMC Genomics</i> , 2017, 18, 877.	2.8	17
58	Quantitative Detection of Individual Cleaved DNA Molecules on Surfaces Using Gold Nanoparticles and Scanning Electron Microscope Imaging. <i>Analytical Chemistry</i> , 2006, 78, 1528-1534.	6.5	16
59	Aldehyde-Terminated Amorphous Carbon Substrates for the Fabrication of Biomolecule Arrays. <i>Langmuir</i> , 2008, 24, 9198-9203.	3.5	16
60	Parallel Detection of Intrinsic Fluorescence from Peptides and Proteins for Quantification during Mass Spectrometric Analysis. <i>Analytical Chemistry</i> , 2011, 83, 2187-2193.	6.5	16
61	Supermolecular Excitation Antenna: Ordered Energy Funnel. <i>Molecular Crystals and Liquid Crystals</i> , 1996, 283, 95-100.	0.3	15
62	Comprehensive in vivo identification of the c-Myc mRNA protein interactome using HyPR-MS. <i>Rna</i> , 2019, 25, 1337-1352.	3.5	15
63	Lifetime Enhancement of Ultrasmall Fluorescent Liquid Polymeric Film Based Optodes by Diffusion-Induced Self-Recovery after Photobleaching. <i>Analytical Chemistry</i> , 1996, 68, 4015-4019.	6.5	14
64	A surface invasive cleavage assay for highly parallel SNP analysis. <i>Human Mutation</i> , 2002, 19, 416-422.	2.5	12
65	HyCCAPP as a tool to characterize promoter DNA-protein interactions in <i>Saccharomyces cerevisiae</i> . <i>Genomics</i> , 2016, 107, 267-273.	2.9	12
66	Elucidating Protein-DNA Interactions in Human Aliphoid Chromatin via Hybridization Capture and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 3433-3442.	3.7	12
67	Proteomic pathways to metabolic disease and type 2 diabetes in the pancreatic islet. <i>IScience</i> , 2021, 24, 103099.	4.1	12
68	Intact-Mass Analysis Facilitating the Identification of Large Human Heart Proteoforms. <i>Analytical Chemistry</i> , 2019, 91, 10937-10942.	6.5	11
69	Comprehensive Detection of Single Amino Acid Variants and Evaluation of Their Deleterious Potential in a PANC-1 Cell Line. <i>Journal of Proteome Research</i> , 2020, 19, 1635-1646.	3.7	11
70	Advanced Strategies for Proton-Transfer Reactions Coupled with Parallel Ion Parking on a 21 T FT-ICR MS for Intact Protein Analysis. <i>Analytical Chemistry</i> , 2021, 93, 9119-9128.	6.5	10
71	Molecular Beacon-Style Hybridization Assay for Quantitative Analysis of Surface Invasive Cleavage Reactions. <i>Analytical Chemistry</i> , 2007, 79, 6031-6036.	6.5	9
72	Back Cover: Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, 1970085.	2.2	9

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73	Precursor Intensity-Based Label-Free Quantification Software Tools for Proteomic and Multi-Omic Analysis within the Galaxy Platform. <i>Proteomes</i> , 2020, 8, 15.	3.5	9
74	Multiplexed Programmable Release of Captured DNA. <i>ChemBioChem</i> , 2014, 15, 2353-2356.	2.6	8
75	Multiplexed Sequence-Specific Capture of Chromatin and Mass Spectrometric Discovery of Associated Proteins. <i>Analytical Chemistry</i> , 2017, 89, 7841-7846.	6.5	8
76	Construction of Human Proteoform Families from 21 Tesla Fourier Transform Ion Cyclotron Resonance Mass Spectrometry Top-Down Proteomic Data. <i>Journal of Proteome Research</i> , 2021, 20, 317-325.	3.7	8
77	Long Noncoding RNAs AC009014.3 and Newly Discovered XPLAID Differentiate Aggressive and Indolent Prostate Cancers. <i>Translational Oncology</i> , 2018, 11, 808-814.	3.7	7
78	A Bayesian Null Interval Hypothesis Test Controls False Discovery Rates and Improves Sensitivity in Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 1975-1981.	3.7	7
79	Mesh Fragmentation Improves Dissociation Efficiency in Top-down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1319-1325.	2.8	7
80	Sirt3 Promotes the Urea Cycle and Fatty Acid Oxidation during Dietary Restriction. <i>Molecular Cell</i> , 2011, 41, 493.	9.7	6
81	Advanced methods for the analysis of chromatin-associated proteins. <i>Physiological Genomics</i> , 2014, 46, 441-447.	2.3	5
82	Revealing the Role of Phosphatidylserine in Shear Stress-Mediated Protection in Endothelial Cells. <i>Endothelium: Journal of Endothelial Cell Research</i> , 2008, 15, 225-230.	1.7	4
83	To understand the whole, you must know the parts: unraveling the roles of protein-DNA interactions in genome regulation. <i>Analyst, The</i> , 2011, 136, 3060.	3.5	4
84	Novel NMR and MS Approaches to Metabolomics. <i>Methods in Pharmacology and Toxicology</i> , 2012, , 199-230.	0.2	4
85	Dendrimeric Antenna Supermolecules with Multistep Directed Energy Transfer. , 1998, , 521-533.		4
86	<title>Anion selective optodes: development of a fluorescent fiber optic sensor for the determination of nitrite activity</title>. , 1996, , .		2
87	MetaNetwork Enhances Biological Insights from Quantitative Proteomics Differences by Combining Clustering and Enrichment Analyses. <i>Journal of Proteome Research</i> , 2022, 21, 410-419.	3.7	2
88	Discovery of Dehydroamino Acid Residues in the Capsid and Matrix Structural Proteins of HIV-1. <i>Journal of Proteome Research</i> , 2022, 21, 993-1001.	3.7	2
89	Molecular Nano-Lenses: Directed Energy Migration and Back-Transfer in Dendrimeric Antenna Supermolecules. <i>Molecular Crystals and Liquid Crystals</i> , 1998, 314, 37-46.	0.3	1
90	Binary Classifier for Computing Posterior Error Probabilities in MetaMorpheus. <i>Journal of Proteome Research</i> , 2021, 20, 1997-2004.	3.7	1

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91	<title>High-throughput single-molecule DNA screening based on electrophoresis</title>., 2000, , .		0
92	Adaptation of Hybridization Capture of Chromatin-associated Proteins for Proteomics to Mammalian Cells. Journal of Visualized Experiments, 2018, , .	0.3	0