

Philip D Compton

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

3,052
citations

186265

28
h-index

189892

50
g-index

61
all docs

61
docs citations

61
times ranked

3096
citing authors

#	ARTICLE	IF	CITATIONS
1	Next-Generation Serology by Mass Spectrometry: Readout of the SARS-CoV-2 Antibody Repertoire. <i>Journal of Proteome Research</i> , 2022, 21, 274-288.	3.7	16
2	Isotopic Resolution of Protein Complexes up to 466 kDa Using Individual Ion Mass Spectrometry. <i>Analytical Chemistry</i> , 2021, 93, 2723-2727.	6.5	32
3	New Interface for Faster Proteoform Analysis: Immunoprecipitation Coupled with SampleStream-Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1659-1670.	2.8	10
4	Spectrum of Apolipoprotein AI and Apolipoprotein AII Proteoforms and Their Associations With Indices of Cardiometabolic Health: The CARDIA Study. <i>Journal of the American Heart Association</i> , 2021, 10, e019890.	3.7	12
5	Novel Interface for High-Throughput Analysis of Biotherapeutics by Electrospray Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 2186-2193.	6.5	28
6	Individual Ion Mass Spectrometry Enhances the Sensitivity and Sequence Coverage of Top-Down Mass Spectrometry. <i>Journal of Proteome Research</i> , 2020, 19, 1346-1350.	3.7	36
7	Voltage Rollercoaster Filtering of Low-Mass Contaminants During Native Protein Analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 763-767.	2.8	8
8	Multiplexed mass spectrometry of individual ions improves measurement of proteoforms and their complexes. <i>Nature Methods</i> , 2020, 17, 391-394.	19.0	110
9	Thorough Performance Evaluation of 213 nm Ultraviolet Photodissociation for Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 405-420.	3.8	38
10	Native vs Denatured: An in Depth Investigation of Charge State and Isotope Distributions. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 574-581.	2.8	27
11	Targeted detection and quantitation of histone modifications from 1,000 cells. <i>PLoS ONE</i> , 2020, 15, e0240829.	2.5	3
12	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
13	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
14	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
15	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
16	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
17	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
18	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0

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19	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
20	STORI Plots Enable Accurate Tracking of Individual Ion Signals. Journal of the American Society for Mass Spectrometry, 2019, 30, 2200-2203.	2.8	44
21	Standard Proteoforms and Their Complexes for Native Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2019, 30, 1190-1198.	2.8	33
22	A novel crosslinking protocol stabilizes amyloid β oligomers capable of inducing Alzheimer's-associated pathologies. Journal of Neurochemistry, 2019, 148, 822-836.	3.9	20
23	Measurement of Individual Ions Sharply Increases the Resolution of Orbitrap Mass Spectra of Proteins. Analytical Chemistry, 2019, 91, 2776-2783.	6.5	57
24	A Targeted, Differential Top-Down Proteomic Methodology for Comparison of ApoA-I Proteoforms in Individuals with High and Low HDL Efflux Capacity. Journal of Proteome Research, 2018, 17, 2156-2164.	3.7	30
25	Mechanism of N_2 Reduction Catalyzed by Fe-Nitrogenase Involves Reductive Elimination of H_2 . Biochemistry, 2018, 57, 701-710.	2.5	80
26	The Ups and Downs of Repeated Cleavage and Internal Fragment Production in Top-Down Proteomics. Journal of the American Society for Mass Spectrometry, 2018, 29, 150-157.	2.8	31
27	Top-down characterization of endogenous protein complexes with native proteomics. Nature Chemical Biology, 2018, 14, 36-41.	8.0	115
28	Estimating the Distribution of Protein Post-Translational Modification States by Mass Spectrometry. Journal of Proteome Research, 2018, 17, 2727-2734.	3.7	33
29	Accurate Sequence Analysis of a Monoclonal Antibody by Top-Down and Middle-Down Orbitrap Mass Spectrometry Applying Multiple Ion Activation Techniques. Analytical Chemistry, 2018, 90, 8421-8429.	6.5	100
30	Chromatographic efficiency and selectivity in top-down proteomics of histones. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2017, 1044-1045, 47-53.	2.3	8
31	Defining Gas-Phase Fragmentation Propensities of Intact Proteins During Native Top-Down Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2017, 28, 1203-1215.	2.8	49
32	Native Electron Capture Dissociation Maps to Iron-Binding Channels in Horse Spleen Ferritin. Analytical Chemistry, 2017, 89, 10711-10716.	6.5	14
33	Advancing Top-down Analysis of the Human Proteome Using a Benchtop Quadrupole-Orbitrap Mass Spectrometer. Journal of Proteome Research, 2017, 16, 609-618.	3.7	68
34	CN-GELFrEE - Clear Native Gel-eluted Liquid Fraction Entrapment Electrophoresis. Journal of Visualized Experiments, 2016, , 53597.	0.3	9
35	Mapping Proteoforms and Protein Complexes From King Cobra Venom Using Both Denaturing and Native Top-down Proteomics. Molecular and Cellular Proteomics, 2016, 15, 2423-2434.	3.8	69
36	An informatic framework for decoding protein complexes by top-down mass spectrometry. Nature Methods, 2016, 13, 237-240.	19.0	59

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37	Targeted analysis of recombinant NF kappa B (RelA/p65) by denaturing and native top down mass spectrometry. <i>Journal of Proteomics</i> , 2016, 134, 76-84.	2.4	10
38	Integrated Bottom-Up and Top-Down Proteomics of Patient-Derived Breast Tumor Xenografts. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 45-56.	3.8	68
39	Unabridged Analysis of Human Histone H3 by Differential Top-Down Mass Spectrometry Reveals Hypermethylated Proteoforms from MMSET/NSD2 Overexpression. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 776-790.	3.8	56
40	Probing asymmetric charge partitioning of protein oligomers during tandem mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2015, 390, 132-136.	1.5	7
41	Native GELFrEE: A New Separation Technique for Biomolecular Assemblies. <i>Analytical Chemistry</i> , 2015, 87, 3032-3038.	6.5	38
42	Reducing protein oxidation in low-flow electrospray enables deeper investigation of proteoforms by top down proteomics. <i>EuPA Open Proteomics</i> , 2015, 8, 40-47.	2.5	8
43	Online Matrix Removal Platform for Coupling Gel-Based Separations to Whole Protein Electrospray Ionization Mass Spectrometry. <i>Journal of Proteome Research</i> , 2015, 14, 2199-2206.	3.7	18
44	Mechanism of Inactivation of GABA Aminotransferase by (<i>Z</i>)-(<i>S</i>)-(<i>S</i>)-3-Amino-4-fluoromethylenyl-1-cyclopentanoic Acid. <i>ACS Chemical Biology</i> , 2015, 10, 2087-2098.	3.4	12
45	Optimizing capillary electrophoresis for top-down proteomics of 30-80 kDa proteins. <i>Proteomics</i> , 2014, 14, 1158-1164.	2.2	76
46	Deep and quantitative top-down proteomics in clinical and translational research. <i>Expert Review of Proteomics</i> , 2014, 11, 649-651.	3.0	35
47	Fragmentation of Integral Membrane Proteins in the Gas Phase. <i>Analytical Chemistry</i> , 2014, 86, 4627-4634.	6.5	25
48	Autopilot: An Online Data Acquisition Control System for the Enhanced High-Throughput Characterization of Intact Proteins. <i>Analytical Chemistry</i> , 2014, 86, 1485-1492.	6.5	33
49	Front-End Electron Transfer Dissociation: A New Ionization Source. <i>Analytical Chemistry</i> , 2013, 85, 8385-8390.	6.5	56
50	Top Down Proteomics of Human Membrane Proteins from Enriched Mitochondrial Fractions. <i>Analytical Chemistry</i> , 2013, 85, 1880-1888.	6.5	72
51	From Protein Complexes to Subunit Backbone Fragments: A Multi-stage Approach to Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 11163-11173.	6.5	148
52	Spinning up mass spectrometry for whole protein complexes. <i>Nature Methods</i> , 2012, 9, 1065-1066.	19.0	14
53	Evaluation of the Compact High-Field Orbitrap for Top-Down Proteomics of Human Cells. <i>Journal of Proteome Research</i> , 2012, 11, 4308-4314.	3.7	84
54	Optimization of Electron Transfer Dissociation via Informed Selection of Reagents and Operating Parameters. <i>Analytical Chemistry</i> , 2012, 84, 1781-1785.	6.5	42

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55	On the Scalability and Requirements of Whole Protein Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 6868-6874.	6.5	177
56	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011, 480, 254-258.	27.8	587
57	Extensive Crosstalk Between O-GlcNAcylation and Phosphorylation Regulates Cytokinesis. <i>Science Signaling</i> , 2010, 3, ra2.	3.6	262
58	Methods for analyzing peptides and proteins on a chromatographic timescale by electron-transfer dissociation mass spectrometry. <i>Nature Protocols</i> , 2008, 3, 1709-1717.	12.0	83