

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	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011, 480, 254-258.	27.8	587
2	Extensive Crosstalk Between O-GlcNAcylation and Phosphorylation Regulates Cytokinesis. <i>Science Signaling</i> , 2010, 3, ra2.	3.6	262
3	On the Scalability and Requirements of Whole Protein Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 6868-6874.	6.5	177
4	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
5	Top-down characterization of endogenous protein complexes with native proteomics. <i>Nature Chemical Biology</i> , 2018, 14, 36-41.	8.0	115
6	Multiplexed mass spectrometry of individual ions improves measurement of proteoforms and their complexes. <i>Nature Methods</i> , 2020, 17, 391-394.	19.0	110
7	Accurate Sequence Analysis of a Monoclonal Antibody by Top-Down and Middle-Down Orbitrap Mass Spectrometry Applying Multiple Ion Activation Techniques. <i>Analytical Chemistry</i> , 2018, 90, 8421-8429.	6.5	100
8	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
9	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
10	Mechanism of N ₂ Reduction Catalyzed by Fe-Nitrogenase Involves Reductive Elimination of H ₂ . <i>Biochemistry</i> , 2018, 57, 701-710.	2.5	80
11	Optimizing capillary electrophoresis for top-down proteomics of 30–80 kDa proteins. <i>Proteomics</i> , 2014, 14, 1158-1164.	2.2	76
12	Top Down Proteomics of Human Membrane Proteins from Enriched Mitochondrial Fractions. <i>Analytical Chemistry</i> , 2013, 85, 1880-1888.	6.5	72
13	Mapping Proteoforms and Protein Complexes From King Cobra Venom Using Both Denaturing and Native Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2423-2434.	3.8	69
14	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
15	Advancing Top-down Analysis of the Human Proteome Using a Benchtop Quadrupole-Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2017, 16, 609-618.	3.7	68
16	An informatic framework for decoding protein complexes by top-down mass spectrometry. <i>Nature Methods</i> , 2016, 13, 237-240.	19.0	59
17	Measurement of Individual Ions Sharply Increases the Resolution of Orbitrap Mass Spectra of Proteins. <i>Analytical Chemistry</i> , 2019, 91, 2776-2783.	6.5	57
18	Front-End Electron Transfer Dissociation: A New Ionization Source. <i>Analytical Chemistry</i> , 2013, 85, 8385-8390.	6.5	56

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19	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
20	Defining Gas-Phase Fragmentation Propensities of Intact Proteins During Native Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 1203-1215.	2.8	49
21	STORI Plots Enable Accurate Tracking of Individual Ion Signals. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2200-2203.	2.8	44
22	Optimization of Electron Transfer Dissociation via Informed Selection of Reagents and Operating Parameters. <i>Analytical Chemistry</i> , 2012, 84, 1781-1785.	6.5	42
23	Native GELFrEE: A New Separation Technique for Biomolecular Assemblies. <i>Analytical Chemistry</i> , 2015, 87, 3032-3038.	6.5	38
24	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
25	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
26	Deep and quantitative top-down proteomics in clinical and translational research. <i>Expert Review of Proteomics</i> , 2014, 11, 649-651.	3.0	35
27	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
28	Estimating the Distribution of Protein Post-Translational Modification States by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 2727-2734.	3.7	33
29	Standard Proteoforms and Their Complexes for Native Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1190-1198.	2.8	33
30	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
31	The Ups and Downs of Repeated Cleavage and Internal Fragment Production in Top-Down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 150-157.	2.8	31
32	A Targeted, Differential Top-Down Proteomic Methodology for Comparison of ApoA-I Proteoforms in Individuals with High and Low HDL Efflux Capacity. <i>Journal of Proteome Research</i> , 2018, 17, 2156-2164.	3.7	30
33	Novel Interface for High-Throughput Analysis of Biotherapeutics by Electrospray Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 2186-2193.	6.5	28
34	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
35	Fragmentation of Integral Membrane Proteins in the Gas Phase. <i>Analytical Chemistry</i> , 2014, 86, 4627-4634.	6.5	25
36	A novel crosslinking protocol stabilizes amyloid β^2 oligomers capable of inducing Alzheimer's associated pathologies. <i>Journal of Neurochemistry</i> , 2019, 148, 822-836.	3.9	20

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37	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
38	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
39	Spinning up mass spectrometry for whole protein complexes. <i>Nature Methods</i> , 2012, 9, 1065-1066.	19.0	14
40	Native Electron Capture Dissociation Maps to Iron-Binding Channels in Horse Spleen Ferritin. <i>Analytical Chemistry</i> , 2017, 89, 10711-10716.	6.5	14
41	Mechanism of Inactivation of GABA Aminotransferase by (<i>Z</i>)-1-(<i>S</i>)-3-(<i>S</i>)-3-Amino-4-fluoromethylenyl-1-cyclopentanoic Acid. <i>ACS Chemical Biology</i> , 2015, 10, 2087-2098.	3.4	12
42	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
43	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
44	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
45	CN-GELFrEE - Clear Native Gel-eluted Liquid Fraction Entrapment Electrophoresis. <i>Journal of Visualized Experiments</i> , 2016, , 53597.	0.3	9
46	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
47	Chromatographic efficiency and selectivity in top-down proteomics of histones. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1044-1045, 47-53.	2.3	8
48	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
49	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
50	Targeted detection and quantitation of histone modifications from 1,000 cells. <i>PLoS ONE</i> , 2020, 15, e0240829.	2.5	3
51	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
52	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
53	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
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58	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0