

# Richard D LeDuc

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

9,958  
citations

218677

26  
h-index

302126

39  
g-index

40  
all docs

40  
docs citations

40  
times ranked

16591  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Blood Proteoform Atlas: A reference map of proteoforms in human hematopoietic cells. <i>Science</i> , 2022, 375, 411-418.	12.6	64
2	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
3	Proteomics Standards Initiativeâ€™s ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. <i>Journal of Proteome Research</i> , 2022, 21, 1189-1195.	3.7	14
4	ProSight Annotator: Complete control and customization of protein entries in UniProt XML files. <i>Proteomics</i> , 2022, 22, e2100209.	2.2	6
5	The Human Proteoform Atlas: a FAIR community resource for experimentally derived proteoforms. <i>Nucleic Acids Research</i> , 2022, 50, D526-D533.	14.5	15
6	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
7	Using 10,000 Fragment Ions to Inform Scoring in Native Top-down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1398-1409.	2.8	18
8	Defining the NSD2 interactome: PARP1 PARylation reduces NSD2 histone methyltransferase activity and impedes chromatin binding. <i>Journal of Biological Chemistry</i> , 2019, 294, 12459-12471.	3.4	16
9	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019, 16, 939-940.	19.0	55
10	Multidimensional Top-Down Proteomics of Brain-Region-Specific Mouse Brain Proteoforms Responsive to Cocaine and Estradiol. <i>Journal of Proteome Research</i> , 2019, 18, 3999-4012.	3.7	12
11	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361.	2.2	147
12	Proteomic analyses of decellularized porcine ovaries identified new matrisome proteins and spatial differences across and within ovarian compartments. <i>Scientific Reports</i> , 2019, 9, 20001.	3.3	39
13	Accurate Estimation of Context-Dependent False Discovery Rates in Top-Down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 796-805.	3.8	27
14	Top-Down Proteomics Enables Comparative Analysis of Brain Proteoforms Between Mouse Strains. <i>Analytical Chemistry</i> , 2018, 90, 3802-3810.	6.5	27
15	Precise characterization of KRAS4b proteoforms in human colorectal cells and tumors reveals mutation/modification cross-talk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4140-4145.	7.1	74
16	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018, 17, 1321-1325.	3.7	35
17	The Value of Activated Ion Electron Transfer Dissociation for High-Throughput Top-Down Characterization of Intact Proteins. <i>Analytical Chemistry</i> , 2018, 90, 8553-8560.	6.5	35
18	High-Throughput Analysis of Intact Human Proteins Using UVPD and HCD on an Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2017, 16, 2072-2079.	3.7	69

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19	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
20	Diversity of Amyloid-beta Proteoforms in the Alzheimer's Disease Brain. <i>Scientific Reports</i> , 2017, 7, 9520.	3.3	125
21	Identification and Characterization of Human Proteoforms by Top-Down LC-21 Tesla FT-ICR Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 1087-1096.	3.7	81
22	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
23	An informatic framework for decoding protein complexes by top-down mass spectrometry. <i>Nature Methods</i> , 2016, 13, 237-240.	19.0	59
24	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
25	A Method for Label-Free, Differential Top-Down Proteomics. <i>Methods in Molecular Biology</i> , 2016, 1410, 121-133.	0.9	27
26	Quantitative Proteomics Reveals Protein-Protein Interactions with Fibroblast Growth Factor 12 as a Component of the Voltage-Gated Sodium Channel 1.2 (Nav1.2) Macromolecular Complex in Mammalian Brain*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1288-1300.	3.8	52
27	Quantitative proteomics and transcriptomics reveals metabolic differences in attracting and non-attracting human-in-mouse glioma stem cell xenografts and stromal cells. <i>EuPA Open Proteomics</i> , 2015, 8, 94-103.	2.5	7
28	ProSight Lite: Graphical software to analyze top-down mass spectrometry data. <i>Proteomics</i> , 2015, 15, 1235-1238.	2.2	196
29	The first pilot project of the consortium for top-down proteomics: <scp>A</scp> status report. <i>Proteomics</i> , 2014, 14, 1130-1140.	2.2	90
30	Applying Label-Free Quantitation to Top Down Proteomics. <i>Analytical Chemistry</i> , 2014, 86, 4961-4968.	6.5	88
31	The C-Score: A Bayesian Framework to Sharply Improve Proteoform Scoring in High-Throughput Top Down Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 3231-3240.	3.7	76
32	Leveraging the national cyberinfrastructure for biomedical research. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2014, 21, 195-199.	4.4	12
33	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013, 8, 1494-1512.	12.0	7,054
34	National Center for Genome Analysis support leverages XSEDE to support life science research. , 2013, , .		3
35	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011, 480, 254-258.	27.8	587
36	Combinatorial Modification of Human Histone H4 Quantitated by Two-dimensional Liquid Chromatography Coupled with Top Down Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2008, 283, 14927-14937.	3.4	164

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37	Using ProSight PTM and Related Tools for Targeted Protein Identification and Characterization with High Mass Accuracy Tandem MS Data. <i>Current Protocols in Bioinformatics</i> , 2007, 19, Unit 13.6.	25.8	38
38	ProSight PTM 2.0: improved protein identification and characterization for top down mass spectrometry. <i>Nucleic Acids Research</i> , 2007, 35, W701-W706.	14.5	222
39	ProSight PTM: an integrated environment for protein identification and characterization by top-down mass spectrometry. <i>Nucleic Acids Research</i> , 2004, 32, W340-W345.	14.5	176
40	ESTIMA, a tool for EST management in a multi-project environment. <i>BMC Bioinformatics</i> , 2004, 5, 176.	2.6	35