

Xiaowen Liu

List of Publications by Year in descending order

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65
papers

2,337
citations

218677

26
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223800

46
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73
docs citations

73
times ranked

2086
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of Machine Learning Models for Proteoform Retention and Migration Time Prediction in Top-Down Mass Spectrometry. <i>Journal of Proteome Research</i> , 2022, 21, 1736-1747.	3.7	2
2	Optimization of protein-level tandem mass tag (TMT) labeling conditions in complex samples with top-down proteomics. <i>Analytica Chimica Acta</i> , 2022, 1221, 340037.	5.4	10
3	Proteoform Identification by Combining RNA-Seq and Top-Down Mass Spectrometry. <i>Journal of Proteome Research</i> , 2021, 20, 261-269.	3.7	7
4	Sorting a Permutation by Best Short Swaps. <i>Algorithmica</i> , 2021, 83, 1953-1979.	1.3	2
5	Quantitative Top-Down Proteomics in Complex Samples Using Protein-Level Tandem Mass Tag Labeling. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1336-1344.	2.8	31
6	TopMSV: A Web-Based Tool for Top-Down Mass Spectrometry Data Visualization. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1312-1318.	2.8	4
7	MASH Explorer: A Universal Software Environment for Top-Down Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 3867-3876.	3.7	62
8	Development of an Online 2D Ultrahigh-Pressure Nano-LC System for High-pH and Low-pH Reversed Phase Separation in Top-Down Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 12774-12777.	6.5	17
9	EnvCNN: A Convolutional Neural Network Model for Evaluating Isotopic Envelopes in Top-Down Mass-Spectral Deconvolution. <i>Analytical Chemistry</i> , 2020, 92, 7778-7785.	6.5	7
10	TopPIC Gateway: A Web Gateway for Top-Down Mass Spectrometry Data Interpretation. , 2020, , .		0
11	Correlation Analysis of Histopathology and Proteogenomics Data for Breast Cancer. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S37-S51.	3.8	24
12	Back Cover: Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, 1970085.	2.2	9
13	Capillary Zone Electrophoresis-Tandem Mass Spectrometry with Activated Ion Electron Transfer Dissociation for Large-scale Top-down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2470-2479.	2.8	17
14	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361.	2.2	147
15	Top-down Mass Spectrometry Analysis of Human Serum Autoantibody Antigen-Binding Fragments. <i>Scientific Reports</i> , 2019, 9, 2345.	3.3	21
16	Large-Scale Qualitative and Quantitative Top-Down Proteomics Using Capillary Zone Electrophoresis-Electrospray Ionization-Tandem Mass Spectrometry with Nanograms of Proteome Samples. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1435-1445.	2.8	41
17	Deep Intact Proteoform Characterization in Human Cell Lysate Using High-pH and Low-pH Reversed-Phase Liquid Chromatography. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2502-2513.	2.8	28
18	A Markov Chain Monte Carlo Method for Estimating the Statistical Significance of Proteoform Identifications by Top-Down Mass Spectrometry. <i>Journal of Proteome Research</i> , 2019, 18, 878-889.	3.7	3

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19	Deep Top-Down Proteomics Using Capillary Zone Electrophoresis-Tandem Mass Spectrometry: Identification of 5700 Proteoforms from the <i>Escherichia coli</i> Proteome. <i>Analytical Chemistry</i> , 2018, 90, 5529-5533.	6.5	95
20	Systematic Evaluation of Protein Sequence Filtering Algorithms for Proteoform Identification Using Top-Down Mass Spectrometry. <i>Proteomics</i> , 2018, 18, 1700306.	2.2	10
21	The Longest Common Exemplar Subsequence Problem. , 2018, , .		2
22	Evaluation of top-down mass spectral identification with homologous protein sequences. <i>BMC Bioinformatics</i> , 2018, 19, 494.	2.6	4
23	Large-scale Top-down Proteomics Using Capillary Zone Electrophoresis Tandem Mass Spectrometry. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	17
24	A graph-based approach for proteoform identification and quantification using top-down homogeneous multiplexed tandem mass spectra. <i>BMC Bioinformatics</i> , 2018, 19, 280.	2.6	3
25	Native Proteomics in Discovery Mode Using Size-Exclusion Chromatography-Capillary Zone Electrophoresis-Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 10095-10099.	6.5	53
26	A mass graph-based approach for the identification of modified proteoforms using top-down tandem mass spectra. <i>Bioinformatics</i> , 2017, 33, 1309-1316.	4.1	30
27	Top-down analysis of immunoglobulin G isotypes 1 and 2 with electron transfer dissociation on a high-field Orbitrap mass spectrometer. <i>Journal of Proteomics</i> , 2017, 159, 67-76.	2.4	47
28	Filling a Protein Scaffold With a Reference. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 123-130.	3.3	2
29	Single-Shot Top-Down Proteomics with Capillary Zone Electrophoresis-Electrospray Ionization-Tandem Mass Spectrometry for Identification of Nearly 600 <i>Escherichia coli</i> Proteoforms. <i>Analytical Chemistry</i> , 2017, 89, 12059-12067.	6.5	75
30	De Novo Sequencing of Peptides from High-Resolution Bottom-Up Tandem Mass Spectra using Top-Down Intended Methods. <i>Proteomics</i> , 2017, 17, 1600321.	2.2	6
31	A spectrum graph-based protein sequence filtering algorithm for proteoform identification by top-down mass spectrometry. , 2017, 2017, 222-229.		5
32	Proteomic Characterization Reveals That MMP-3 Correlates With Bronchiolitis Obliterans Syndrome Following Allogeneic Hematopoietic Cell and Lung Transplantation. <i>American Journal of Transplantation</i> , 2016, 16, 2342-2351.	4.7	32
33	Characterization of Proteoforms with Unknown Post-translational Modifications Using the MIScore. <i>Journal of Proteome Research</i> , 2016, 15, 2422-2432.	3.7	22
34	Top-down analysis of protein samples by <i>de novo</i> sequencing techniques. <i>Bioinformatics</i> , 2016, 32, 2753-2759.	4.1	14
35	TopPIC: a software tool for top-down mass spectrometry-based proteoform identification and characterization. <i>Bioinformatics</i> , 2016, 32, 3495-3497.	4.1	179
36	MASH Suite Pro: A Comprehensive Software Tool for Top-Down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 703-714.	3.8	111

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37	SpectroGene: A Tool for Proteogenomic Annotations Using Top-Down Spectra. <i>Journal of Proteome Research</i> , 2016, 15, 144-151.	3.7	14
38	Filling a Protein Scaffold with a Reference. <i>Lecture Notes in Computer Science</i> , 2016, , 175-186.	1.3	0
39	De Novo Sequencing of Peptides from Top-Down Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2015, 14, 4450-4462.	3.7	31
40	Identification of Glycopeptides with Multiple Hydroxylysine O-Glycosylation Sites by Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2015, 14, 5099-5108.	3.7	13
41	An efficient algorithm for the blocked pattern matching problem. <i>Bioinformatics</i> , 2015, 31, 532-538.	4.1	11
42	A new scoring function for top-down spectral deconvolution. <i>BMC Genomics</i> , 2014, 15, 1140.	2.8	12
43	Spectral probabilities of top-down tandem mass spectra. <i>BMC Genomics</i> , 2014, 15, S9.	2.8	14
44	Top-down Proteomics Reveals Concerted Reductions in Myofilament and Z-disc Protein Phosphorylation after Acute Myocardial Infarction. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2752-2764.	3.8	96
45	De Novo Protein Sequencing by Combining Top-Down and Bottom-Up Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2014, 13, 3241-3248.	3.7	51
46	Quantitative analysis of human salivary gland-derived intact proteome using top-down mass spectrometry. <i>Proteomics</i> , 2014, 14, 1211-1222.	2.2	44
47	Improving protein order-disorder classification using charge-hydrophathy plots. <i>BMC Bioinformatics</i> , 2014, 15, S4.	2.6	63
48	Top-down proteomics reveals a unique protein S-thiolation switch in <i>Salmonella</i> Typhimurium in response to infection-like conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10153-10158.	7.1	140
49	Identification of Ultramodified Proteins Using Top-Down Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2013, 12, 5830-5838.	3.7	47
50	Identification of Ultramodified Proteins Using Top-Down Spectra. <i>Lecture Notes in Computer Science</i> , 2013, , 132-144.	1.3	2
51	Protein Identification Using Top-Down Spectra. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.008524.	3.8	127
52	Speeding up tandem mass spectral identification using indexes. <i>Bioinformatics</i> , 2012, 28, 1692-1697.	4.1	12
53	Dereplicating nonribosomal peptides using an informatic search algorithm for natural products (iSNAP) discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19196-19201.	7.1	62
54	Better score function for peptide identification with ETD MS/MS spectra. <i>BMC Bioinformatics</i> , 2010, 11, S4.	2.6	26

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55	Deconvolution and Database Search of Complex Tandem Mass Spectra of Intact Proteins. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2772-2782.	3.8	145
56	Modeling Protein Interacting Groups by Quasi-Biclques: Complexity, Algorithm, and Application. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 354-364.	3.0	28
57	Automated protein (re)sequencing with MS/MS and a homologous database yields almost full coverage and accuracy. <i>Bioinformatics</i> , 2009, 25, 2174-2180.	4.1	33
58	Approximation Algorithms for Biclustering Problems. <i>SIAM Journal on Computing</i> , 2008, 38, 1504-1518.	1.0	4
59	A $(1.5 + \hat{\mu})$ -Approximation Algorithm for Unsigned Translocation Distance. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 56-66.	3.0	12
60	An Efficient Voting Algorithm for Finding Additive Biclusters with Random Background. <i>Journal of Computational Biology</i> , 2008, 15, 1275-1293.	1.6	4
61	Quasi-biclques: Complexity and Binding Pairs. <i>Lecture Notes in Computer Science</i> , 2008, , 255-264.	1.3	16
62	Finding Additive Biclusters with Random Background. , 2008, , 263-276.		1
63	Computing the maximum similarity bi-clusters of gene expression data. <i>Bioinformatics</i> , 2007, 23, 50-56.	4.1	142
64	Finding the region of pseudo-periodic tandem repeats in biological sequences. <i>Algorithms for Molecular Biology</i> , 2006, 1, 2.	1.2	8
65	http://www.elsevier.com/locate/0959-2688(06)00001-2 <small>xmlns:xs="http://www.w3.org/2001/XMLSchema" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://www.elsevier.com/xml/ja/dtd" xmlns:ja="http://www.elsevier.com/xml/ja/dtd" xmlns:mml="http://www.w3.org/1998/Math/MathML" xmlns:tb="http://www.elsevier.com/xml/common/table/dtd" xmlns:sb="http://www.elsevier.com/xml/common/struct-bib/dtd" xmlns:ce="http://www.elsevier.com/x</small>	1.2	31