

Luca Fornelli

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/638366/publications.pdf>

Version: 2024-02-01

53
papers

2,973
citations

182225

30
h-index

198040

52
g-index

57
all docs

57
docs citations

57
times ranked

3222
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.	6.0	64
2	Characterization of large intact protein ions by mass spectrometry: What directions should we follow?. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2022, 1870, 140758.	1.1	11
3	Structural and Functional Characterization of a Novel Scorpion Toxin that Inhibits NaV1.8 via Interactions With the DI Voltage Sensor and DII Pore Module. <i>Frontiers in Pharmacology</i> , 2022, 13, .	1.6	2
4	Sequential Ion-Ion Reactions for Enhanced Gas-Phase Sequencing of Large Intact Proteins in a Tribrid Orbitrap Mass Spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 2334-2345.	1.2	19
5	Mass spectrometry-based proteomic platforms for better understanding of SARS-CoV-2 induced pathogenesis and potential diagnostic approaches. <i>Proteomics</i> , 2021, 21, e2000279.	1.3	19
6	Oncogenic KRAS creates an aspartate metabolism signature in colorectal cancer cells. <i>FEBS Journal</i> , 2021, 288, 6683-6699.	2.2	7
7	Identification and Characterization of Novel Proteins from Arizona Bark Scorpion Venom That Inhibit Nav1.8, a Voltage-Gated Sodium Channel Regulator of Pain Signaling. <i>Toxins</i> , 2021, 13, 501.	1.5	4
8	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.	1.6	12
9	Evolutionary Dynamics of Indels in SARS-CoV-2 Spike Glycoprotein. <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432110646.	0.6	5
10	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.	1.2	67
11	Thorough Performance Evaluation of 213 nm Ultraviolet Photodissociation for Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 405-420.	2.5	38
12	Elucidating Proteoform Dynamics Underlying the Senescence Associated Secretory Phenotype. <i>Journal of Proteome Research</i> , 2020, 19, 938-948.	1.8	8
13	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.	1.6	16
14	Direct measurement of light and heavy antibody chains using ion mobility and middle-down mass spectrometry. <i>MAbs</i> , 2019, 11, 1351-1357.	2.6	22
15	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019, 16, 587-594.	9.0	241
16	Proton Transfer Charge Reduction Enables High-Throughput Top-Down Analysis of Large Proteoforms. <i>Analytical Chemistry</i> , 2019, 91, 15732-15739.	3.2	45
17	Structural Analysis of Monoclonal Antibodies by Ultrahigh Resolution MALDI In-Source Decay FT-ICR Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 2079-2085.	3.2	48
18	A comprehensive pipeline for translational top-down proteomics from a single blood draw. <i>Nature Protocols</i> , 2019, 14, 119-152.	5.5	62

#	ARTICLE	IF	CITATIONS
19	Precise characterization of KRAS4b proteoforms in human colorectal cells and tumors reveals mutation/modification cross-talk. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4140-4145.	3.3	74
20	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.	1.8	30
21	Chemical-Mediated Digestion: An Alternative Realm for Middle-down Proteomics?. Journal of Proteome Research, 2018, 17, 2005-2016.	1.8	12
22	Top-down proteomics: Where we are, where we are going?. Journal of Proteomics, 2018, 175, 3-4.	1.2	47
23	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.	1.2	31
24	Top-down characterization of endogenous protein complexes with native proteomics. Nature Chemical Biology, 2018, 14, 36-41.	3.9	115
25	Multiplexed Middle-Down Mass Spectrometry as a Method for Revealing Light and Heavy Chain Connectivity in a Monoclonal Antibody. Analytical Chemistry, 2018, 90, 12527-12535.	3.2	38
26	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.	3.2	100
27	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.	1.2	8
28	Top-down analysis of immunoglobulin G isotypes 1 and 2 with electron transfer dissociation on a high-field Orbitrap mass spectrometer. Journal of Proteomics, 2017, 159, 67-76.	1.2	47
29	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.	1.2	49
30	Advancing Top-down Analysis of the Human Proteome Using a Benchtop Quadrupole-Orbitrap Mass Spectrometer. Journal of Proteome Research, 2017, 16, 609-618.	1.8	68
31	Bioinformatics Analysis of Top-Down Mass Spectrometry Data with ProSight Lite. Methods in Molecular Biology, 2017, 1558, 381-394.	0.4	27
32	Progress in Top-Down Proteomics and the Analysis of Proteoforms. Annual Review of Analytical Chemistry, 2016, 9, 499-519.	2.8	427
33	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.	2.5	69
34	An informatic framework for decoding protein complexes by top-down mass spectrometry. Nature Methods, 2016, 13, 237-240.	9.0	59
35	Quantitation and Identification of Thousands of Human Proteoforms below 30 kDa. Journal of Proteome Research, 2016, 15, 976-982.	1.8	89
36	Targeted analysis of recombinant NF kappa B (RelA/p65) by denaturing and native top down mass spectrometry. Journal of Proteomics, 2016, 134, 76-84.	1.2	10

#	ARTICLE	IF	CITATIONS
37	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.	2.5	56
38	Ion Coalescence in Fourier Transform Mass Spectrometry: Should We Worry about This in Shotgun Proteomics?. <i>European Journal of Mass Spectrometry</i> , 2015, 21, 459-470.	0.5	14
39	Probing asymmetric charge partitioning of protein oligomers during tandem mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2015, 390, 132-136.	0.7	7
40	Distinguishing Analyte from Noise Components in Mass Spectra of Complex Samples: Where to Cut the Noise?. <i>Analytical Chemistry</i> , 2014, 86, 3308-3316.	3.2	44
41	Advantages of Extended Bottom-Up Proteomics Using Sap9 for Analysis of Monoclonal Antibodies. <i>Analytical Chemistry</i> , 2014, 86, 9945-9953.	3.2	50
42	Middle-Down Analysis of Monoclonal Antibodies with Electron Transfer Dissociation Orbitrap Fourier Transform Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 3005-3012.	3.2	147
43	Top-down analysis of 30-80 kDa proteins by electron transfer dissociation time-of-flight mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 8505-8514.	1.9	34
44	Principles of electron capture and transfer dissociation mass spectrometry applied to peptide and protein structure analysis. <i>Chemical Society Reviews</i> , 2013, 42, 5014.	18.7	175
45	Practical Considerations for Improving the Productivity of Mass Spectrometry-based Proteomics. <i>Chimia</i> , 2013, 67, 244.	0.3	10
46	Analysis of Intact Monoclonal Antibody IgG1 by Electron Transfer Dissociation Orbitrap FTMS. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1758-1767.	2.5	137
47	In-Spray Supercharging of Peptides and Proteins in Electrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 4647-4651.	3.2	74
48	Observation of ion coalescence in Orbitrap Fourier transform mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 1711-1717.	0.7	65
49	Glycan variability on a recombinant IgG antibody transiently produced in HEK-293E cells. <i>New Biotechnology</i> , 2012, 29, 471-476.	2.4	28
50	Structural Analysis of Intact Monoclonal Antibodies by Electron Transfer Dissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 8919-8927.	3.2	121
51	High-Resolution and Tandem Mass Spectrometry – the Indispensable Tools of the XXI Century. <i>Chimia</i> , 2011, 65, 641.	0.3	4
52	Deamidation and Transamidation of Substance P by Tissue Transglutaminase Revealed by Electron Capture Dissociation Fourier Transform Mass Spectrometry. <i>Chemistry - A European Journal</i> , 2011, 17, 486-497.	1.7	13
53	Inside Cover: Deamidation and Transamidation of Substance P by Tissue Transglutaminase Revealed by Electron Capture Dissociation Fourier Transform Mass Spectrometry (Chem. Eur. J. 2/2011). <i>Chemistry - A European Journal</i> , 2011, 17, 398-398.	1.7	0