Catherine Fenselau

List of Publications by Year in descending order

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88 papers

6,630 citations

38 h-index 78 g-index

88 all docs 88 docs citations

88 times ranked 6405 citing authors

#	Article	IF	CITATIONS
1	Proteolytic 180 Labeling for Comparative Proteomics: Â Model Studies with Two Serotypes of Adenovirus. Analytical Chemistry, 2001, 73, 2836-2842.	3.2	807
2	Characterization of intact microorganisms by MALDI mass spectrometry. Mass Spectrometry Reviews, 2001, 20, 157-171.	2.8	750
3	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214.	3.9	580
4	Myeloid-Derived Suppressor Cells: Immune-Suppressive Cells That Impair Antitumor Immunity and Are Sculpted by Their Environment. Journal of Immunology, 2018, 200, 422-431.	0.4	404
5	Characterization of the Protein Subset Desorbed by MALDI from Whole Bacterial Cells. Analytical Chemistry, 2001, 73, 746-750.	3.2	325
6	Microorganism Identification by Mass Spectrometry and Protein Database Searches. Analytical Chemistry, 1999, 71, 2732-2738.	3.2	307
7	Dissection of Proteolytic 18O Labeling: Â Endoprotease-Catalyzed 16O-to-18O Exchange of Truncated Peptide Substrates. Journal of Proteome Research, 2003, 2, 147-152.	1.8	199
8	Proteolytic18O Labeling for Comparative Proteomics: Evaluation of Endoprotease Glu-C as the Catalytic Agentâ€. Journal of Proteome Research, 2002, 1, 27-33.	1.8	169
9	Rapid Characterization of Spores of Bacillus cereus Group Bacteria by Matrix-Assisted Laser Desorption-lonization Time-of-Flight Mass Spectrometry. Applied and Environmental Microbiology, 2000, 66, 3828-3834.	1.4	141
10	Kurstakins:Â A New Class of Lipopeptides Isolated fromBacillusthuringiensis. Journal of Natural Products, 2000, 63, 1492-1496.	1.5	137
11	Exosomes from Myeloid-Derived Suppressor Cells Carry Biologically Active Proteins. Journal of Proteome Research, 2014, 13, 836-843.	1.8	137
12	Characterization of Protein Biomarkers Desorbed by MALDI from Whole Fungal Cells. Analytical Chemistry, 2001, 73, 5228-5231.	3.2	121
13	Lectin-Based Affinity Capture for MALDI-MS Analysis of Bacteria. Analytical Chemistry, 1999, 71, 1460-1463.	3.2	117
14	Identification of Bacillus Spores by Matrix-Assisted Laser Desorption Ionization–Mass Spectrometry. Applied and Environmental Microbiology, 1999, 65, 4313-4319.	1.4	113
15	Structural analysis of oligosaccharides by tandem mass spectrometry: Collisional activation of sodium adduct ions. Biological Mass Spectrometry, 1990, 19, 747-754.	0.5	102
16	Lectin and Carbohydrate Affinity Capture Surfaces for Mass Spectrometric Analysis of Microorganisms. Analytical Chemistry, 2001, 73, 751-757.	3. 2	97
17	A review of quantitative methods for proteomic studies. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 855, 14-20.	1.2	93
18	Small, Acid-Soluble Proteins as Biomarkers in Mass Spectrometry Analysis of Bacillu s Spores. Applied and Environmental Microbiology, 2003, 69, 1100-1107.	1.4	90

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19	18O2-Labeling in Quantitative Proteomic Strategies: A Status Report. Journal of Proteome Research, 2009, 8, 2140-2143.	1.8	88
20	Mass Spectrometry-Based Proteolytic Mapping for Rapid Virus Identification. Analytical Chemistry, 2002, 74, 2529-2534.	3.2	84
21	Differential Content of Proteins, mRNAs, and miRNAs Suggests that MDSC and Their Exosomes May Mediate Distinct Immune Suppressive Functions. Journal of Proteome Research, 2018, 17, 486-498.	1.8	84
22	Investigation of Doxorubicin Resistance in MCF-7 Breast Cancer Cells Using Shot-Gun Comparative Proteomics with Proteolytic18O Labeling. Journal of Proteome Research, 2004, 3, 455-462.	1.8	82
23	High-Throughput Middle-Down Analysis Using an Orbitrap. Journal of Proteome Research, 2010, 9, 3886-3890.	1.8	78
24	Characterization ofBacillusSpore Species and Their Mixtures Using Postsource Decay with a Curved-Field Reflectron. Analytical Chemistry, 2003, 75, 5618-5627.	3.2	70
25	Integration of Jacobson's Pellicle Method into Proteomic Strategies for Plasma Membrane Proteins. Journal of Proteome Research, 2004, 3, 1267-1277.	1.8	69
26	Rapid Chemical Digestion of Small Acid-Soluble Spore Proteins for Analysis ofBacillusSpores. Analytical Chemistry, 2006, 78, 181-188.	3.2	63
27	Evaluation of Microwave-Accelerated Residue-Specific Acid Cleavage for Proteomic Applications. Journal of Proteome Research, 2008, 7, 579-586.	1.8	62
28	Analysis of Viral Glycoproteins by MALDI-TOF Mass Spectrometry. Analytical Chemistry, 2001, 73, 1544-1548.	3.2	59
29	The PRY/SPRY/B30.2 Domain of Butyrophilin 1A1 (BTN1A1) Binds to Xanthine Oxidoreductase. Journal of Biological Chemistry, 2009, 284, 22444-22456.	1.6	59
30	Surface Glycoproteins of Exosomes Shed by Myeloid-Derived Suppressor Cells Contribute to Function. Journal of Proteome Research, 2017, 16, 238-246.	1.8	57
31	Rapid characterization ofBacillus spores targeting species-unique peptides produced with an atmospheric pressure matrix-assisted laser desorption/ionization source. Journal of Mass Spectrometry, 2005, 40, 464-474.	0.7	53
32	Unbiased Examination of Changes in Plasma Membrane Proteins in Drug Resistant Cancer Cells. Journal of Proteome Research, 2005, 4, 2148-2153.	1.8	53
33	Differential Protein Expression in the Cytosol Fraction of an MCF-7 Breast Cancer Cell Line Selected for Resistance toward Melphalan. Journal of Proteome Research, 2002, 1, 435-442.	1.8	50
34	A Duplicated ESAT-6 Region of ESX-5 Is Involved in Protein Export and Virulence of Mycobacteria. Infection and Immunity, 2015, 83, 4349-4361.	1.0	49
35	Ubiquitinated Proteins in Exosomes Secreted by Myeloid-Derived Suppressor Cells. Journal of Proteome Research, 2014, 13, 5965-5972.	1.8	44
36	Rapid microorganism identification with on-slide proteolytic digestion followed by matrix-assisted laser desorption/ionization tandem mass spectrometry and database searching. Rapid Communications in Mass Spectrometry, 2002, 16, 1953-1956.	0.7	42

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37	Applications of $1.06 \cdot \hat{1}$ /4m IR Laser Desorption on a Fourier Transform Mass Spectrometer. Analytical Chemistry, 1998, 70, 4890-4895.	3.2	41
38	Extracellular vesicle proteomes reflect developmental phases of Bacillus subtilis. Clinical Proteomics, 2016, 13, 6.	1.1	41
39	Corona plasma discharge for rapid analysis of microorganisms by mass spectrometry. , 1999, 13, 604-606.		38
40	Primary sequence and siteâ€selective hydroxylation of prolines in isoforms of a major peanut allergen protein Ara h 2. Protein Science, 2010, 19, 174-182.	3.1	38
41	Analysis of a Model Virus Using Residue-Specific Chemical Cleavage and MALDI-TOF Mass Spectrometry. Analytical Chemistry, 2007, 79, 654-658.	3.2	36
42	Top–down analysis of low mass proteins in exosomes shed by murine myeloid-derived suppressor cells. International Journal of Mass Spectrometry, 2015, 378, 264-269.	0.7	34
43	Integration of Residue-Specific Acid Cleavage into Proteomic Workflows. Journal of Proteome Research, 2007, 6, 4525-4527.	1.8	33
44	Factors contributing to peak broadening and mass accuracy in the characterization of intact spores using matrix-assisted laser desorption/ionization coupled with time-of-flight mass spectrometry. Journal of Mass Spectrometry, 2001, 36, 929-936.	0.7	30
45	Proteomic Evidence for Roles for Nucleolin and Poly[ADP-ribosyl] Transferase in Drug Resistance. Journal of Proteome Research, 2005, 4, 1583-1591.	1.8	29
46	Endothermic ion molecule reactions. Journal of the American Society for Mass Spectrometry, 1991, 2, 189-197.	1.2	25
47	Identification of β-Lactamase in Antibiotic-Resistant <i>Bacillus cereus</i> Spores. Applied and Environmental Microbiology, 2008, 74, 904-906.	1.4	25
48	Matrix-assisted laser desorption/ionization time-of-flight analysis of Bacillus spores using a 2.94?i¿½ minfrared laser. Rapid Communications in Mass Spectrometry, 2000, 14, 1701-1706.	0.7	24
49	Integration of 180 Labeling and Solution Isoelectric Focusing in a Shotgun Analysis of Mitochondrial Proteins. Journal of Proteome Research, 2007, 6, 4601-4607.	1.8	24
50	Detection of Plasmid Insertion in Escherichia coliby MALDI-TOF Mass Spectrometry. Analytical Chemistry, 2007, 79, 5399-5406.	3.2	24
51	Enrichment of Plasma Membrane Proteins Using Nanoparticle Pellicles: Comparison between Silica and Higher Density Nanoparticles. Journal of Proteome Research, 2013, 12, 1134-1141.	1.8	23
52	Critical Reviews in Analytical Chemistry. Analytical Chemistry, 2014, 86, 1-1.	3.2	22
53	Solution Isoelectric Focusing for Peptide Analysis:Â Comparative Investigation of an Insoluble Nuclear Protein Fraction. Journal of Proteome Research, 2005, 4, 2126-2132.	1.8	20
54	Extension of microwave-accelerated residue-specific acid cleavage to proteins with carbohydrate side chains and disulfide linkages. International Journal of Mass Spectrometry, 2008, 278, 109-113.	0.7	20

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55	Evaluation of Spectral Counting for Relative Quantitation of Proteoforms in Top-Down Proteomics. Analytical Chemistry, 2016, 88, 10900-10907.	3.2	18
56	Proteolytic Labeling With 18O for Comparative Proteomics Studies. Methods in Molecular Biology, 2007, 359, 135-142.	0.4	18
57	Molecular cargo in myeloid-derived suppressor cells and their exosomes. Cellular Immunology, 2021, 359, 104258.	1.4	17
58	Proteomic Identification and Analysis of K63-Linked Ubiquitin Conjugates. Analytical Chemistry, 2012, 84, 10121-10128.	3.2	16
59	Unexpected Trypsin Cleavage at Ubiquitinated Lysines. Analytical Chemistry, 2015, 87, 8144-8148.	3.2	16
60	Peptideâ€based systems analysis of inflammation induced myeloidâ€derived suppressor cells reveals diverse signaling pathways. Proteomics, 2016, 16, 1881-1888.	1.3	16
61	Microwave assisted acid cleavage for denaturation and proteolysis of intact human adenovirus. International Journal of Mass Spectrometry, 2011, 301, 7-11.	0.7	14
62	Top-Down Proteomic Characterization of Truncated Proteoforms. Journal of Proteome Research, 2019, 18, 4013-4019.	1.8	14
63	Ubiquitin Conjugation Probed by Inflammation in Myeloid-Derived Suppressor Cell Extracellular Vesicles. Journal of Proteome Research, 2018, 17, 315-324.	1.8	13
64	Rapid analysis of ricin using hot acid digestion and MALDIâ€TOF mass spectrometry. Journal of Mass Spectrometry, 2018, 53, 1013-1017.	0.7	13
65	Top-Down Analysis of Branched Proteins Using Mass Spectrometry. Analytical Chemistry, 2018, 90, 4032-4038.	3.2	12
66	Massâ€biased partitioning to enhance middle down proteomics analysis. Journal of Mass Spectrometry, 2013, 48, 340-343.	0.7	10
67	Characterization of intact microorganisms by MALDI mass spectrometry., 2001, 20, 157.		10
68	Quantitative Protein Analysis Using Enzymatic [¹⁸ 0]Water Labeling. Current Protocols in Protein Science, 2014, 76, 23.4.1-23.4.9.	2.8	9
69	Metastable decay of peptide ions on a Fourier transform mass spectrometer equipped with an external ion source., 2000, 35, 183-188.		8
70	Preparing to read the ubiquitin code: top-down analysis of unanchored ubiquitin tetramers. Journal of Mass Spectrometry, 2016, 51, 629-637.	0.7	8
71	Preparing to read the ubiquitin code: characterization of ubiquitin trimers by topâ€down mass spectrometry. Journal of Mass Spectrometry, 2016, 51, 315-321.	0.7	8
72	Preparing to read the ubiquitin code: a middleâ€out strategy for characterization of all lysineâ€linked diubiquitins. Journal of Mass Spectrometry, 2014, 49, 1272-1278.	0.7	7

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73	Microwave supported hydrolysis prepares Bacillus spores for proteomic analysis. International Journal of Mass Spectrometry, 2019, 435, 227-233.	0.7	7
74	MALDI-TOF Mass Spectrometric Detection of SARS-CoV-2 Using Cellulose Sulfate Ester Enrichment and Hot Acid Treatment. Journal of Proteome Research, 2022, 21, 2055-2062.	1.8	7
75	Analysis of the topology of ubiquitin chains. Methods in Enzymology, 2019, 626, 323-346.	0.4	6
76	Topâ€down analysis of novel synthetic branched proteins. Journal of Mass Spectrometry, 2019, 54, 19-25.	0.7	6
77	Rapid Characterization of Microorganisms by Mass Spectrometry: An Overview. ACS Symposium Series, 2011, , 1-4.	0.5	4
78	Laser Desorption electron impact mass spectrometry: Studies of ion radical fragmentation mechanisms and hydrogen/deuterium rearrangement in time-resolved experiments. Organic Mass Spectrometry, 1989, 24, 694-698.	1.3	3
79	Nanowire pellicles for eukaryotic cells: nanowire coating and interaction with cells. Nanomedicine, 2014, 9, 1171-1180.	1.7	2
80	Extraction of Membrane Components from Neisseria gonorrhoeae Using Catanionic Surfactant Vesicles: A New Approach for the Study of Bacterial Surface Molecules. Pharmaceutics, 2020, 12, 787.	2.0	2
81	Bioinformatics for Flexibility, Reliability, and Mixture Analysis of Intact Microorganisms. , 2006, , 257-277.		1
82	Asp-Selective Microwave-Supported Acid Proteolysis. , 2013, , 225-236.		1
83	Comparison of nanowire pellicles for plasma membrane enrichment: coating nanowires on cell. Journal of Nanoparticle Research, 2013, 15, 2133.	0.8	1
84	Corona plasma discharge for rapid analysis of microorganisms by mass spectrometry., 1999, 13, 604.		1
85	Isotope Labeling in Quantitative Proteomics. , 2006, , 47-61.		0
86	From genes to function: Kick-starting US HUPO. Journal of Proteomics, 2014, 107, 144-145.	1.2	0
87	Application of Higher Density Iron Oxide Nanoparticle Pellicles to Enrich the Plasma Membrane and Its Proteome from Cells in Suspension. Methods in Molecular Biology, 2018, 1722, 79-90.	0.4	O
88	Catherine Clarke Fenselau. , 2015, , 75-76.		0