

Daniel A Figeys

List of Publications by Year in descending order

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236
papers

16,062
citations

22153

59
h-index

20358

116
g-index

267
all docs

267
docs citations

267
times ranked

18254
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic identification of protein complexes in <i>Saccharomyces cerevisiae</i> by mass spectrometry. <i>Nature</i> , 2002, 415, 180-183.	27.8	3,445
2	Large-scale mapping of human protein-protein interactions by mass spectrometry. <i>Molecular Systems Biology</i> , 2007, 3, 89.	7.2	850
3	Lab-on-a-Chip: A Revolution in Biological and Medical Sciences.. <i>Analytical Chemistry</i> , 2000, 72, 330 A-335 A.	6.5	478
4	Altered intestinal microbiota-host mitochondria crosstalk in new onset Crohn's disease. <i>Nature Communications</i> , 2016, 7, 13419.	12.8	326
5	18O Labeling: a tool for proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 2456-2465.	1.5	318
6	Quantitative analysis of SARS-CoV-2 RNA from wastewater solids in communities with low COVID-19 incidence and prevalence. <i>Water Research</i> , 2021, 188, 116560.	11.3	297
7	Identification of Flow-dependent Endothelial Nitric-oxide Synthase Phosphorylation Sites by Mass Spectrometry and Regulation of Phosphorylation and Nitric Oxide Production by the Phosphatidylinositol 3-Kinase Inhibitor LY294002. <i>Journal of Biological Chemistry</i> , 1999, 274, 30101-30108.	3.4	296
8	A Microfabricated Device for Rapid Protein Identification by Microelectrospray Ion Trap Mass Spectrometry. <i>Analytical Chemistry</i> , 1997, 69, 3153-3160.	6.5	222
9	Metaproteomics reveals associations between microbiome and intestinal extracellular vesicle proteins in pediatric inflammatory bowel disease. <i>Nature Communications</i> , 2018, 9, 2873.	12.8	209
10	RapidAIM: a culture- and metaproteomics-based Rapid Assay of Individual Microbiome responses to drugs. <i>Microbiome</i> , 2020, 8, 33.	11.1	209
11	The functional diversity of protein lysine methylation. <i>Molecular Systems Biology</i> , 2014, 10, 724.	7.2	202
12	Proteomics on a chip: Promising developments. <i>Electrophoresis</i> , 2001, 22, 208-216.	2.4	199
13	Protein identification by solid phase microextraction-capillary zone electrophoresis-microelectrospray-tandem mass spectrometry. <i>Nature Biotechnology</i> , 1996, 14, 1579-1583.	17.5	183
14	Advancing functional and translational microbiome research using meta-omics approaches. <i>Microbiome</i> , 2019, 7, 154.	11.1	177
15	The Tale of Two Domains. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 560-572.	3.8	168
16	Lipidomics era: Accomplishments and challenges. <i>Mass Spectrometry Reviews</i> , 2010, 29, 877-929.	5.4	161
17	Catching a resurgence: Increase in SARS-CoV-2 viral RNA identified in wastewater 48h before COVID-19 clinical tests and 96h before hospitalizations. <i>Science of the Total Environment</i> , 2021, 770, 145319.	8.0	159
18	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155

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19	MetaPro-IQ: a universal metaproteomic approach to studying human and mouse gut microbiota. <i>Microbiome</i> , 2016, 4, 31.	11.1	154
20	Protein Identification by Capillary Zone Electrophoresis/Microelectrospray Ionization-Tandem Mass Spectrometry at the Subfemtomole Level. <i>Analytical Chemistry</i> , 1996, 68, 1822-1828.	6.5	143
21	Proteome analysis: Biological assay or data archive?. <i>Electrophoresis</i> , 1998, 19, 1862-1871.	2.4	141
22	An Integrated Microfluidics-Tandem Mass Spectrometry System for Automated Protein Analysis. <i>Analytical Chemistry</i> , 1998, 70, 3728-3734.	6.5	140
23	Nanoflow Solvent Gradient Delivery from a Microfabricated Device for Protein Identifications by Electrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 1998, 70, 3721-3727.	6.5	128
24	MetaLab: an automated pipeline for metaproteomic data analysis. <i>Microbiome</i> , 2017, 5, 157.	11.1	128
25	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. <i>Cancer Cell</i> , 2022, 40, 70-87.e15.	16.8	120
26	Assessing the impact of protein extraction methods for human gut metaproteomics. <i>Journal of Proteomics</i> , 2018, 180, 120-127.	2.4	115
27	Identification of proteins by capillary electrophoresis-tandem mass spectrometry evaluation of an on-line solid-phase extraction device. <i>Journal of Chromatography A</i> , 1997, 763, 295-306.	3.7	113
28	Proteomics: from Gel Based to Gel Free. <i>Analytical Chemistry</i> , 2005, 77, 3771-3788.	6.5	104
29	Proteomic analyses of the SMYD family interactomes identify HSP90 as a novel target for SMYD2. <i>Journal of Molecular Cell Biology</i> , 2011, 3, 301-308.	3.3	103
30	Functional Dissection of the NuA4 Histone Acetyltransferase Reveals Its Role as a Genetic Hub and that Eaf1 Is Essential for Complex Integrity. <i>Molecular and Cellular Biology</i> , 2008, 28, 2244-2256.	2.3	101
31	High sensitivity analysis of proteins and peptides by capillary electrophoresis-tandem mass spectrometry: Recent developments in technology and applications. <i>Electrophoresis</i> , 1998, 19, 885-892.	2.4	100
32	Proteomics in 2002: A Year of Technical Development and Wide-Ranging Applications. <i>Analytical Chemistry</i> , 2003, 75, 2891-2905.	6.5	97
33	Proteomic Analysis of Ubiquitinated Proteins from Human MCF-7 Breast Cancer Cells by Immunoaffinity Purification and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2005, 4, 2192-2200.	3.7	95
34	A Novel Proteomics Approach for the Discovery of Chromatin-associated Protein Networks. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 870-882.	3.8	95
35	Mass Spectrometry for the Study of Protein-Protein Interactions. <i>Methods</i> , 2001, 24, 230-239.	3.8	93
36	Adapting arrays and lab-on-a-chip technology for proteomics. <i>Proteomics</i> , 2002, 2, 373.	2.2	93

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37	Electrophoresis combined with novel mass spectrometry techniques: Powerful tools for the analysis of proteins and proteomes. <i>Electrophoresis</i> , 1998, 19, 1811-1818.	2.4	91
38	Missense Mutation in APOC3 within the C-terminal Lipid Binding Domain of Human ApoC-III Results in Impaired Assembly and Secretion of Triacylglycerol-rich Very Low Density Lipoproteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 27769-27780.	3.4	91
39	Identification of novel lipid droplet factors that regulate lipophagy and cholesterol efflux in macrophage foam cells. <i>Autophagy</i> , 2021, 17, 3671-3689.	9.1	90
40	HysTag—A Novel Proteomic Quantification Tool Applied to Differential Display Analysis of Membrane Proteins From Distinct Areas of Mouse Brain. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 82-92.	3.8	88
41	The Proteomic Reactor:—A Microfluidic Device for Processing Minute Amounts of Protein Prior to Mass Spectrometry Analysis. <i>Journal of Proteome Research</i> , 2006, 5, 2754-2759.	3.7	88
42	Two-Color Cell Array Screen Reveals Interdependent Roles for Histone Chaperones and a Chromatin Boundary Regulator in Histone Gene Repression. <i>Molecular Cell</i> , 2009, 35, 340-351.	9.7	88
43	Î2-Catenin and NF-ÎB co-activation triggered by TLR3 stimulation facilitates stem cell-like phenotypes in breast cancer. <i>Cell Death and Differentiation</i> , 2015, 22, 298-310.	11.2	87
44	PINK1-mediated phosphorylation of LETM1 regulates mitochondrial calcium transport and protects neurons against mitochondrial stress. <i>Nature Communications</i> , 2017, 8, 1399.	12.8	87
45	Activation of the Cdc42p GTPase by cyclin-dependent protein kinases in budding yeast. <i>EMBO Journal</i> , 2007, 26, 4487-4500.	7.8	84
46	Metabolic Reprogramming by Hexosamine Biosynthetic and Golgi N-Glycan Branching Pathways. <i>Scientific Reports</i> , 2016, 6, 23043.	3.3	84
47	Deep Metaproteomics Approach for the Study of Human Microbiomes. <i>Analytical Chemistry</i> , 2017, 89, 9407-9415.	6.5	83
48	High sensitivity identification of proteins by electrospray ionization tandem mass spectrometry: Initial comparison between an ion trap mass spectrometer and a triple quadrupole mass spectrometer. <i>Electrophoresis</i> , 1997, 18, 360-368.	2.4	81
49	Advancements in Top-Down Proteomics. <i>Analytical Chemistry</i> , 2012, 84, 720-734.	6.5	80
50	Death-associated Protein 4 Binds MST1 and Augments MST1-induced Apoptosis. <i>Journal of Biological Chemistry</i> , 2002, 277, 47991-48001.	3.4	79
51	Use of the fluorescent intercalating dyes POPO-3, YOYO-3 and YOYO-1 for ultrasensitive detection of double-stranded DNA separated by capillary electrophoresis with hydroxypropylmethyl cellulose and non-cross-linked polyacrylamide. <i>Journal of Chromatography A</i> , 1994, 669, 205-216.	3.7	78
52	Tryptic digestion of ubiquitin standards reveals an improved strategy for identifying ubiquitinated proteins by mass spectrometry. <i>Proteomics</i> , 2007, 7, 868-874.	2.2	76
53	Mapping protein—protein interactions by mass spectrometry. <i>Current Opinion in Biotechnology</i> , 2006, 17, 394-399.	6.6	72
54	An in vitro model maintaining taxon-specific functional activities of the gut microbiome. <i>Nature Communications</i> , 2019, 10, 4146.	12.8	70

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55	A Regulatory Network Involving β -Catenin, e-Cadherin, PI3k/Akt, and Slug Balances Self-Renewal and Differentiation of Human Pluripotent Stem Cells In Response to Wnt Signaling. <i>Stem Cells</i> , 2015, 33, 1419-1433.	3.2	69
56	Proteomic analysis of ascending colon biopsies from a paediatric inflammatory bowel disease inception cohort identifies protein biomarkers that differentiate Crohn's disease from UC. <i>Gut</i> , 2017, 66, 1573-1583.	12.1	69
57	Biomarker Assay Translation from Discovery to Clinical Studies in Cancer Drug Development: Quantification of Emerging Protein Biomarkers. <i>Advances in Cancer Research</i> , 2006, 96, 269-298.	5.0	68
58	Exploring the effects of operational mode and microbial interactions on bacterial community assembly in a one-stage partial-nitritation anammox reactor using integrated multi-omics. <i>Microbiome</i> , 2019, 7, 122.	11.1	65
59	Amyloid- β signals tau hyperphosphorylation and compromises neuronal viability by disrupting alkylacylglycerophosphocholine metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20936-20941.	7.1	64
60	iMetaLab 1.0: a web platform for metaproteomics data analysis. <i>Bioinformatics</i> , 2018, 34, 3954-3956.	4.1	64
61	Data-Dependent Modulation of Solid-Phase Extraction Capillary Electrophoresis for the Analysis of Complex Peptide and Phosphopeptide Mixtures by Tandem Mass Spectrometry: An Application to Endothelial Nitric Oxide Synthase. <i>Analytical Chemistry</i> , 1999, 71, 2279-2287.	6.5	63
62	Exploring the Yeast Acetylome Using Functional Genomics. <i>Cell</i> , 2012, 149, 936-948.	28.9	63
63	The Proteomic Landscape of the Suprachiasmatic Nucleus Clock Reveals Large-Scale Coordination of Key Biological Processes. <i>PLoS Genetics</i> , 2014, 10, e1004695.	3.5	63
64	Perspective and Guidelines for Metaproteomics in Microbiome Studies. <i>Journal of Proteome Research</i> , 2019, 18, 2370-2380.	3.7	63
65	An enhanced microfluidic chip coupled to an electrospray Qstar mass spectrometer for protein identification. <i>Electrophoresis</i> , 2000, 21, 181-190.	2.4	62
66	Using neurolipidomics to identify phospholipid mediators of synaptic (dys)function in Alzheimer's Disease. <i>Frontiers in Physiology</i> , 2013, 4, 168.	2.8	60
67	Optimization of solid phase microextraction - capillary zone electrophoresis - mass spectrometry for high sensitivity protein identification. <i>Electrophoresis</i> , 1998, 19, 2338-2347.	2.4	58
68	Defining the budding yeast chromatin-associated interactome. <i>Molecular Systems Biology</i> , 2010, 6, 448.	7.2	58
69	Nonsynonymous Mutations within APOB in Human Familial Hypobetalipoproteinemia. <i>Journal of Biological Chemistry</i> , 2010, 285, 6453-6464.	3.4	58
70	Proteomics in 2005/2006: Developments, Applications and Challenges. <i>Analytical Chemistry</i> , 2007, 79, 4325-4344.	6.5	57
71	Improvement of the Quantification Accuracy and Throughput for Phosphoproteome Analysis by a Pseudo Triplex Stable Isotope Dimethyl Labeling Approach. <i>Analytical Chemistry</i> , 2011, 83, 7755-7762.	6.5	57
72	Large-scale characterization of intact N-glycopeptides using an automated glycoproteomic method. <i>Journal of Proteomics</i> , 2014, 110, 145-154.	2.4	57

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73	Quantitative site-specific ADP-ribosylation profiling of DNA-dependent PARPs. <i>DNA Repair</i> , 2015, 30, 68-79.	2.8	56
74	Functional analysis of the missense APOC3 mutation Ala23Thr associated with human hypotriglyceridemia. <i>Journal of Lipid Research</i> , 2010, 51, 1524-1534.	4.2	53
75	Rare Cell Proteomic Reactor Applied to Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)-based Quantitative Proteomics Study of Human Embryonic Stem Cell Differentiation. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S10.	3.8	52
76	BAG2 Gene-mediated Regulation of PINK1 Protein Is Critical for Mitochondrial Translocation of PARKIN and Neuronal Survival. <i>Journal of Biological Chemistry</i> , 2015, 290, 30441-30452.	3.4	52
77	Bottom-Up Proteomics (2013-2015): Keeping up in the Era of Systems Biology. <i>Analytical Chemistry</i> , 2016, 88, 95-121.	6.5	52
78	Activation energy of single-stranded DNA moving through cross-linked polyacrylamide gels at 300 V/cm effect of temperature on sequencing rate in high-electric-field capillary gel electrophoresis. <i>Journal of Chromatography A</i> , 1994, 680, 503-510.	3.7	51
79	Lipin - The bridge between hepatic glycerolipid biosynthesis and lipoprotein metabolism. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2010, 1801, 1249-1259.	2.4	51
80	Techniques for the Optimization of Proteomic Strategies Based on Head Column Stacking Capillary Electrophoresis. <i>Analytical Chemistry</i> , 2000, 72, 2684-2689.	6.5	50
81	The Liver Connexin32 Interactome Is a Novel Plasma Membrane-Mitochondrial Signaling Nexus. <i>Journal of Proteome Research</i> , 2013, 12, 2597-2610.	3.7	45
82	miR-132/212 Modulates Seasonal Adaptation and Dendritic Morphology of the Central Circadian Clock. <i>Cell Reports</i> , 2017, 19, 505-520.	6.4	45
83	Microfabricated device coupled with an electrospray ionization quadrupole time-of-flight mass spectrometer: protein identifications based on enhanced-resolution mass spectrometry and tandem mass spectrometry data. <i>Rapid Communications in Mass Spectrometry</i> , 1998, 12, 1435-1444.	1.5	44
84	Mapping the human protein interactome. <i>Cell Research</i> , 2008, 18, 716-724.	12.0	44
85	Proteomic and Metaproteomic Approaches to Understand Host-Microbe Interactions. <i>Analytical Chemistry</i> , 2018, 90, 86-109.	6.5	44
86	A novel whole-cell lysate kinase assay identifies substrates of the p38 MAPK in differentiating myoblasts. <i>Skeletal Muscle</i> , 2012, 2, 5.	4.2	43
87	Proteomics: From Technology Developments to Biological Applications. <i>Analytical Chemistry</i> , 2009, 81, 4585-4599.	6.5	42
88	DJ-1 Interacts with and Regulates Paraoxonase-2, an Enzyme Critical for Neuronal Survival in Response to Oxidative Stress. <i>PLoS ONE</i> , 2014, 9, e106601.	2.5	42
89	Comparison of different search engines using validated MS/MS test datasets. <i>Analytica Chimica Acta</i> , 2005, 534, 11-20.	5.4	41
90	Evaluating in Vitro Culture Medium of Gut Microbiome with Orthogonal Experimental Design and a Metaproteomics Approach. <i>Journal of Proteome Research</i> , 2018, 17, 154-163.	3.7	41

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91	Novel approaches to map protein interactions. <i>Current Opinion in Biotechnology</i> , 2003, 14, 119-125.	6.6	40
92	Restriction of histone gene transcription to S phase by phosphorylation of a chromatin boundary protein. <i>Genes and Development</i> , 2011, 25, 2489-2501.	5.9	40
93	Site-specific characterization of cell membrane N-glycosylation with integrated hydrophilic interaction chromatography solid phase extraction and LC-MS/MS. <i>Journal of Proteomics</i> , 2014, 103, 194-203.	2.4	40
94	<i>In Vitro</i> Metabolic Labeling of Intestinal Microbiota for Quantitative Metaproteomics. <i>Analytical Chemistry</i> , 2016, 88, 6120-6125.	6.5	40
95	Capillary electrophoresis of peptides and proteins at neutral pH in capillaries covalently coated with polyethyleneimine. <i>Biomedical Applications</i> , 1997, 695, 163-168.	1.7	38
96	Recent developments in mass spectrometry-based quantitative phosphoproteomics This paper is one of a selection of papers published in this Special Issue, entitled CSBMCB " Systems and Chemical Biology, and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2008, 86, 137-148.	2.0	38
97	Targeted lipidomics " advances in profiling lysophosphocholine and platelet-activating factor second messengers. <i>FEBS Journal</i> , 2013, 280, 5652-5667.	4.7	38
98	mChIP-KAT-MS, a method to map protein interactions and acetylation sites for lysine acetyltransferases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1641-50.	7.1	38
99	The Proteomic Reactor Facilitates the Analysis of Affinity-Purified Proteins by Mass Spectrometry: An Application for Identifying Ubiquitinated Proteins in Human Cells. <i>Journal of Proteome Research</i> , 2007, 6, 298-305.	3.7	37
100	Technological developments in lipidomics. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 7, 395-409.	3.8	37
101	Pink1 regulates FKBP5 interaction with AKT/PHLPP and protects neurons from neurotoxin stress induced by MPP+. <i>Journal of Neurochemistry</i> , 2019, 150, 312-329.	3.9	37
102	Nanoflow Gradient Generator Coupled with H^+ -LC-ESI-MS/MS for Protein Identification. <i>Analytical Chemistry</i> , 2001, 73, 1307-1315.	6.5	36
103	On-line strong cation exchange H^+ -HPLC-ESI-MS/MS for protein identification and process optimization. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 719-727.	2.8	36
104	Proteomics technology in systems biology. <i>Molecular BioSystems</i> , 2006, 2, 364.	2.9	35
105	The tryptophan-rich domain of purolidine is directly associated with the starch granule surface as judged by tryptic shaving and mass spectrometry. <i>Journal of Cereal Science</i> , 2010, 52, 115-120.	3.7	35
106	Skeletal myosin light chain kinase regulates skeletal myogenesis by phosphorylation of MEF2C. <i>EMBO Journal</i> , 2011, 30, 2477-2489.	7.8	35
107	Phosphoproteome Profiling Reveals Circadian Clock Regulation of Posttranslational Modifications in the Murine Hippocampus. <i>Frontiers in Neurology</i> , 2017, 8, 110.	2.4	35
108	Development of a Multiplexed Microfluidic Proteomic Reactor and Its Application for Studying Protein-Protein Interactions. <i>Analytical Chemistry</i> , 2011, 83, 4095-4102.	6.5	34

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109	Regulation of the VHL/HIF-1 Pathway by DJ-1. <i>Journal of Neuroscience</i> , 2014, 34, 8043-8050.	3.6	34
110	Discovery of Substrates for a SET Domain Lysine Methyltransferase Predicted by Multistate Computational Protein Design. <i>Structure</i> , 2015, 23, 206-215.	3.3	34
111	Definition and Characterization of a α -Trypsinosome from Specific Peptide Characteristics by Nano-HPLC ^{MS/MS} and in Silico Analysis of Complex Protein Mixtures. <i>Journal of Proteome Research</i> , 2004, 3, 1138-1148.	3.7	33
112	Regulation of Septin Dynamics by the <i>Saccharomyces cerevisiae</i> Lysine Acetyltransferase NuA4. <i>PLoS ONE</i> , 2011, 6, e25336.	2.5	33
113	Proteomic reactors and their applications in biology. <i>FEBS Journal</i> , 2011, 278, 3796-3806.	4.7	33
114	Microsome-associated luminal lipid droplets in the regulation of lipoprotein secretion. <i>Current Opinion in Lipidology</i> , 2013, 24, 160-170.	2.7	33
115	Multiplexed Proteomic Reactor for the Processing of Proteomic Samples. <i>Analytical Chemistry</i> , 2007, 79, 39-44.	6.5	32
116	Widespread protein lysine acetylation in gut microbiome and its alterations in patients with Crohn's disease. <i>Nature Communications</i> , 2020, 11, 4120.	12.8	32
117	Lysoform fragment ions facilitate the determination of stereospecificity of diacyl glycerophospholipids. <i>Rapid Communications in Mass Spectrometry</i> , 2011, 25, 205-217.	1.5	31
118	Improved Recovery and Identification of Membrane Proteins from Rat Hepatic Cells using a Centrifugal Proteomic Reactor. <i>Molecular and Cellular Proteomics</i> , 2011, 10, O111.008425.	3.8	31
119	Quantitative proteomic analysis of <i>Dunaliella salina</i> upon acute arsenate exposure. <i>Chemosphere</i> , 2016, 145, 112-118.	8.2	31
120	Peer Reviewed: Prometrics Approaches in Drug Discovery. <i>Analytical Chemistry</i> , 2002, 74, 412 A-419 A.	6.5	30
121	A charge-suppressing strategy for probing protein methylation. <i>Chemical Communications</i> , 2016, 52, 5474-5477.	4.1	30
122	Berberine and its structural analogs have differing effects on functional profiles of individual gut microbiomes. <i>Gut Microbes</i> , 2020, 11, 1348-1361.	9.8	30
123	Mobility of single-stranded DNA as a function of cross-linker concentration in polyacrylamide capillary gel electrophoresis. <i>Journal of Chromatography A</i> , 1993, 645, 311-317.	3.7	29
124	Ras Binding Triggers Ubiquitination of the Ras Exchange Factor Ras-GRF2. <i>Molecular and Cellular Biology</i> , 2001, 21, 2107-2117.	2.3	29
125	Combining different 'omics' technologies to map and validate protein-protein interactions in humans. <i>Briefings in Functional Genomics & Proteomics</i> , 2004, 2, 357-365.	3.8	29
126	Glycoproteomic Reactor for Human Plasma. <i>Journal of Proteome Research</i> , 2009, 8, 556-566.	3.7	29

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127	Analytical Aspects of Proteomics: 2009–2010. <i>Analytical Chemistry</i> , 2011, 83, 4407-4426.	6.5	28
128	From Cells to Peptides: One-Stop Integrated Proteomic Processing Using Amphipols. <i>Journal of Proteome Research</i> , 2013, 12, 1512-1519.	3.7	28
129	Gelsolin regulates cisplatin sensitivity in human head-and-neck cancer. <i>International Journal of Cancer</i> , 2014, 135, 2760-2769.	5.1	28
130	Methylmercury can induce Parkinson's-like neurotoxicity similar to 1-methyl-4-phenylpyridinium: a genomic and proteomic analysis on MN9D dopaminergic neuron cells. <i>Journal of Toxicological Sciences</i> , 2015, 40, 817-828.	1.5	28
131	Metaproteomic and Metabolomic Approaches for Characterizing the Gut Microbiome. <i>Proteomics</i> , 2019, 19, e1800363.	2.2	28
132	Identification and Quantitation of Changes in the Platelet Activating Factor Family of Glycerophospholipids over the Course of Neuronal Differentiation by High-Performance Liquid Chromatography Electrospray Ionization Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2007, 79, 8539-8548.	6.5	26
133	Uncovering the Proteome Response of the Master Circadian Clock to Light Using an AutoProteome System. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.007252.	3.8	26
134	High throughput solid phase microextraction: A new alternative for analysis of cellular lipidome?. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1043, 12-19.	2.3	26
135	Analysis of the Subcellular Phosphoproteome Using a Novel Phosphoproteomic Reactor. <i>Journal of Proteome Research</i> , 2010, 9, 1279-1288.	3.7	25
136	A New Chemical Probe for Phosphatidylinositol Kinase Activity. <i>ChemBioChem</i> , 2014, 15, 1253-1256.	2.6	25
137	Therapeutic Targeting of Casein Kinase 1 β in an Alzheimer's Disease Mouse Model. <i>Journal of Proteome Research</i> , 2019, 18, 3383-3393.	3.7	25
138	Aging Disrupts the Circadian Patterns of Protein Expression in the Murine Hippocampus. <i>Frontiers in Aging Neuroscience</i> , 2019, 11, 368.	3.4	25
139	Open: Mucosal-luminal interface proteomics reveals biomarkers of pediatric inflammatory bowel disease-associated colitis. <i>American Journal of Gastroenterology</i> , 2018, 113, 713-724.	0.4	23
140	A Differential Phosphoproteomic Analysis of Retinoic Acid-Treated P19 Cells. <i>Journal of Proteome Research</i> , 2007, 6, 3174-3186.	3.7	22
141	The reproducible acquisition of comparative liquid chromatography/tandem mass spectrometry data from complex biological samples. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 1697-1710.	1.5	21
142	MetaLab 2.0 Enables Accurate Post-Translational Modifications Profiling in Metaproteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1473-1482.	2.8	21
143	Proteomic analysis of minute amount of colonic biopsies by enteroscopy sampling. <i>Biochemical and Biophysical Research Communications</i> , 2016, 476, 286-292.	2.1	20
144	Fine Tuning of Proteomic Technologies to Improve Biological Findings: Advancements in 2011–2013. <i>Analytical Chemistry</i> , 2014, 86, 176-195.	6.5	18

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145	Spatial and temporal depletion of ions from noncrosslinked denaturing polyacrylamide in capillary electrophoresis. <i>Electrophoresis</i> , 1994, 15, 1512-1517.	2.4	17
146	Analysis of protein interaction networks using mass spectrometry compatible techniques. <i>Analytica Chimica Acta</i> , 2006, 564, 10-18.	5.4	17
147	Phosphoproteome analysis of an early onset mouse model (<sc>T</sc>g<sc>CRND</sc>8) of <sc>A</sc>zheimer's disease reveals temporal changes in neuronal and glia signaling pathways. <i>Proteomics</i> , 2013, 13, 1292-1305.	2.2	17
148	APols-Aided Protein Precipitation: A Rapid Method for Concentrating Proteins for Proteomic Analysis. <i>Journal of Membrane Biology</i> , 2014, 247, 941-947.	2.1	17
149	GRK2 Fine-Tunes Circadian Clock Speed and Entrainment via Transcriptional and Post-translational Control of PERIOD Proteins. <i>Cell Reports</i> , 2015, 12, 1272-1288.	6.4	17
150	MFG-E8 Is Critical for Embryonic Stem Cell-Mediated T Cell Immunomodulation. <i>Stem Cell Reports</i> , 2015, 5, 741-752.	4.8	17
151	Quantitative phosphoproteomics reveals involvement of multiple signaling pathways in early phagocytosis by the retinal pigmented epithelium. <i>Journal of Biological Chemistry</i> , 2017, 292, 19826-19839.	3.4	17
152	Co-targeting Bulk Tumor and CSCs in Clinically Translatable TNBC Patient-Derived Xenografts via Combination Nanotherapy. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 1755-1764.	4.1	17
153	Multiple separations of DNA sequencing fragments with a non-cross-linked polyacrylamide-filled capillary: capillary electrophoresis at 300 V/cm. <i>Journal of Chromatography A</i> , 1995, 717, 113-116.	3.7	16
154	Analysis of low-abundance proteins using the proteomic reactor with pH fractionation. <i>Talanta</i> , 2010, 80, 1526-1531.	5.5	16
155	Highly sensitive detection of S-nitrosylated proteins by capillary gel electrophoresis with laser induced fluorescence. <i>Journal of Chromatography A</i> , 2011, 1218, 6756-6762.	3.7	16
156	Pseudo-coulmetric loading in capillary electrophoresis DNA sequencing. <i>Journal of Chromatography A</i> , 1996, 744, 325-331.	3.7	15
157	Quantitative Proteomic Analysis of PCSK9 Gain of Function in Human Hepatic HuH7 Cells. <i>Journal of Proteome Research</i> , 2011, 10, 2011-2026.	3.7	15
158	A functional ecological network based on metaproteomics responses of individual gut microbiomes to resistant starches. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3833-3842.	4.1	15
159	Identification of lysophosphatidylcholine (LPC) and platelet activating factor (PAF) from PC12 cells and mouse cortex using liquid chromatography/multi-stage mass spectrometry (LC/MS³). <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 3579-3587.	1.5	14
160	Mass Spectrometric Analysis Reveals Remnants of Host-Pathogen Molecular Interactions at the Starch Granule Surface in Wheat Endosperm. <i>Phytopathology</i> , 2010, 100, 848-854.	2.2	14
161	Combination of online enzyme digestion with stable isotope labeling for high-throughput quantitative proteome analysis. <i>Proteomics</i> , 2012, 12, 3129-3137.	2.2	14
162	17β-Estradiol results in a proprotein convertase subtilisin/kexin type 9-dependent increase in low-density lipoprotein receptor levels in human hepatic HuH7 cells. <i>FEBS Journal</i> , 2015, 282, 2682-2696.	4.7	14

#	ARTICLE	IF	CITATIONS
163	Proteomic Analysis of Cerebellum in Common Marmoset Exposed to Methylmercury. <i>Toxicological Sciences</i> , 2015, 146, 43-51.	3.1	14
164	N-Glycopeptide Reduction with Exoglycosidases Enables Accurate Characterization of Site-Specific N-Glycosylation. <i>Analytical Chemistry</i> , 2016, 88, 11837-11843.	6.5	14
165	Peptide-Centric Approaches Provide an Alternative Perspective To Re-Examine Quantitative Proteomic Data. <i>Analytical Chemistry</i> , 2016, 88, 1973-1978.	6.5	14
166	Associations Between Soluble LDLR and Lipoproteins in a White Cohort and the Effect of PCSK9 Loss-of-Function. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 3486-3495.	3.6	14
167	Phospholipase C Activity Affinity Purifies with the Torpedo Nicotinic Acetylcholine Receptor. <i>Journal of Biological Chemistry</i> , 2010, 285, 10337-10343.	3.4	13
168	Myosin Phosphatase Modulates the Cardiac Cell Fate by Regulating the Subcellular Localization of Nrx2.5 in a Wnt/Rho-Associated Protein Kinase-Dependent Pathway. <i>Circulation Research</i> , 2013, 112, 257-266.	4.5	13
169	Platelet activating factors are associated with depressive symptoms in coronary artery disease patients: a hypothesis-generating study. <i>Neuropsychiatric Disease and Treatment</i> , 2015, 11, 2309.	2.2	13
170	Detergent-Assisted Glycoprotein Capture: A Versatile Tool for In-Depth N-Glycoproteome Analysis. <i>Journal of Proteome Research</i> , 2016, 15, 2080-2086.	3.7	13
171	Proteomics and Metaproteomics Add Functional, Taxonomic and Biomass Dimensions to Modeling the Ecosystem at the Mucosal-luminal Interface. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1409-1417.	3.8	13
172	PCSK4-null sperm display enhanced protein tyrosine phosphorylation and ADAM2 proteolytic processing during in vitro capacitation. <i>Fertility and Sterility</i> , 2010, 93, 1112-1123.	1.0	12
173	Srf1 Is a Novel Regulator of Phospholipase D Activity and Is Essential to Buffer the Toxic Effects of C16:0 Platelet Activating Factor. <i>PLoS Genetics</i> , 2011, 7, e1001299.	3.5	12
174	Visualization and Phospholipid Identification (VaLID): online integrated search engine capable of identifying and visualizing glycerophospholipids with given mass. <i>Bioinformatics</i> , 2013, 29, 284-285.	4.1	12
175	Development of Online pH Gradient-Eluted Strong Cation Exchange Nanoelectrospray-Tandem Mass Spectrometry for Proteomic Analysis Facilitating Basic and Histidine-Containing Peptides Identification. <i>Analytical Chemistry</i> , 2016, 88, 583-591.	6.5	12
176	Proteome profiling reveals regional protein alteration in cerebrum of common marmoset (<i>Callithrix</i>). <i>Journal of Proteome Research</i> , 2014, 13, 1075-1084.	4.2	11
177	Chemoenzymatic Method for Glycoproteomic N-Glycan Type Quantitation. <i>Analytical Chemistry</i> , 2020, 92, 1618-1627.	6.5	11
178	New ammunition for the proteomic reactor: strong anion exchange beads and multiple enzymes enhance protein identification and sequence coverage. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 397, 3421-3430.	3.7	10
179	Analysis of human serum phosphopeptidome by a focused database searching strategy. <i>Journal of Proteomics</i> , 2013, 78, 389-397.	2.4	10
180	Time-of-Day- and Light-Dependent Expression of Ubiquitin Protein Ligase E3 Component N-Recognin 4 (UBR4) in the Suprachiasmatic Nucleus Circadian Clock. <i>PLoS ONE</i> , 2014, 9, e103103.	2.5	10

#	ARTICLE	IF	CITATIONS
181	Shedding of cancer susceptibility candidate 4 by the convertases PC7/furin unravels a novel secretory protein implicated in cancer progression. <i>Cell Death and Disease</i> , 2020, 11, 665.	6.3	10
182	Functional proteomics: mapping protein-protein interactions and pathways. <i>Current Opinion in Molecular Therapeutics</i> , 2002, 4, 210-5.	2.8	10
183	Labeling of Double-Stranded DNA by ROX-Dideoxycytosine Triphosphate Using Terminal Deoxynucleotidyl Transferase and Separation by Capillary Electrophoresis. <i>Analytical Chemistry</i> , 1994, 66, 4382-4383.	6.5	9
184	Effect of the age of non-cross-linked polyacrylamide on the separation of DNA sequencing samples. <i>Journal of Chromatography A</i> , 1995, 717, 105-111.	3.7	9
185	Systematic determination of ion score cutoffs based on calculated false positive rates: application for identifying ubiquitinated proteins by tandem mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2008, 43, 296-304.	1.6	9
186	Identification of Lysines within Membrane-Anchored Mga2p120 that Are Targets of Rsp5p Ubiquitination and Mediate Mobilization of Tethered Mga2p90. <i>Journal of Molecular Biology</i> , 2009, 385, 718-725.	4.2	9
187	An enhanced chemically defined SILAC culture system for quantitative proteomics study of human embryonic stem cells. <i>Proteomics</i> , 2011, 11, 4040-4046.	2.2	9
188	Detecting Protein-Protein Interactions/Complex Components Using Mass Spectrometry Coupled Techniques. <i>Methods in Molecular Biology</i> , 2014, 1164, 1-13.	0.9	9
189	Solvation of the proton and the trifluoromethanesulfonate ion in eight solvents. <i>Canadian Journal of Chemistry</i> , 1991, 69, 1985-1988.	1.1	8
190	Enthalpies of solution of naphthalene, N,N-dimethyl-1-naphthylamine, and 1,8-bis(dimethylamino)naphthalene in 16 organic solvents. <i>Canadian Journal of Chemistry</i> , 1992, 70, 1586-1589.	1.1	8
191	Identification of Protein-Protein Interactions by Mass Spectrometry Coupled Techniques. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2008, 110, 67-80.	1.1	8
192	The precursor to the germ cell-specific PCSK4 proteinase is inefficiently activated in transfected somatic cells: evidence of interaction with the BiP chaperone. <i>Molecular and Cellular Biochemistry</i> , 2011, 348, 43-52.	3.1	8
193	Platelet-activating factors are associated with cognitive deficits in depressed coronary artery disease patients: a hypothesis-generating study. <i>Journal of Neuroinflammation</i> , 2014, 11, 119.	7.2	8
194	Comparative proteomic analysis reveals metabolic variability of probiotic <i>Enterococcus durans</i> during aerobic and anaerobic cultivation. <i>Journal of Proteomics</i> , 2020, 220, 103764.	2.4	8
195	Purification of Trypsin for Mass Spectrometric Identification of Proteins at High Sensitivity. <i>Analytical Biochemistry</i> , 1998, 261, 124-127.	2.4	7
196	Profiling Kinase Activity during Hepatitis C Virus Replication Using a Wortmannin Probe. <i>ACS Infectious Diseases</i> , 2015, 1, 443-452.	3.8	7
197	Differential proteomic analysis of synovial fluid from hip arthroplasty patients with a pseudotumor vs. Periprosthetic osteolysis. <i>Journal of Orthopaedic Research</i> , 2018, 36, 1849-1859.	2.3	7
198	pepFunk: a tool for peptide-centric functional analysis of metaproteomic human gut microbiome studies. <i>Bioinformatics</i> , 2020, 36, 4171-4179.	4.1	7

#	ARTICLE	IF	CITATIONS
199	Metaproteomics Reveals Growth Phase-Dependent Responses of an <i>In Vitro</i> Gut Microbiota to Metformin. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1448-1458.	2.8	7
200	Evaluating live microbiota biobanking using an <i>ex vivo</i> microbiome assay and metaproteomics. <i>Gut Microbes</i> , 2022, 14, 2035658.	9.8	7
201	iMetaLab Suite: A one-stop toolset for metaproteomics. , 2022, 1, .		7
202	Strategy to Design Improved Proteomic Experiments Based on Statistical Analyses of the Chemical Properties of Identified Peptides. <i>Journal of Proteome Research</i> , 2005, 4, 2201-2206.	3.7	6
203	Activity-based profiling of the proteasome pathway during hepatitis C virus infection. <i>Proteomics</i> , 2015, 15, 3815-3825.	2.2	6
204	A non-canonical monovalent zinc finger stabilizes the integration of Cfp1 into the H3K4 methyltransferase complex COMPASS. <i>Nucleic Acids Research</i> , 2020, 48, 421-431.	14.5	6
205	Exploring the Microbiome-Wide Lysine Acetylation, Succinylation, and Propionylation in Human Gut Microbiota. <i>Analytical Chemistry</i> , 2021, 93, 6594-6598.	6.5	6
206	Change in conductivity in non-cross-linked polyacrylamide capillary electrophoresis Effects of aging polyacrylamide and buffer composition. <i>Journal of Chromatography A</i> , 1996, 744, 333-339.	3.7	5
207	Differential Proteomic Screen To Evidence Proteins Ubiquitinated upon Mitotic Exit in Cell-Free Extract of <i>Xenopus laevis</i> Embryos. <i>Journal of Proteome Research</i> , 2008, 7, 4701-4714.	3.7	5
208	Studying the Temporal Dynamics of the Gut Microbiota Using Metabolic Stable Isotope Labeling and Metaproteomics. <i>Analytical Chemistry</i> , 2020, 92, 15711-15718.	6.5	5
209	MealTime-MS: A Machine Learning-Guided Real-Time Mass Spectrometry Analysis for Protein Identification and Efficient Dynamic Exclusion. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1459-1472.	2.8	5
210	Examining the Effects of an Anti-Salmonella Bacteriophage Preparation, BAFASALÂ®, on Ex-Vivo Human Gut Microbiome Composition and Function Using a Multi-Omics Approach. <i>Viruses</i> , 2021, 13, 1734.	3.3	5
211	Structural analysis of <i>Atopobium parvulum</i> SufS cysteine desulfurase linked to Crohn's disease. <i>FEBS Letters</i> , 2022, 596, 898-909.	2.8	5
212	Of proteins and DNA's proteomic role in the field of chromatin research. <i>Molecular BioSystems</i> , 2010, 6, 30-37.	2.9	4
213	Separation and characterization of human microbiomes by metaproteomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2018, 108, 221-230.	11.4	4
214	Differential Lysis Approach Enables Selective Extraction of Taxon-Specific Proteins for Gut Metaproteomics. <i>Analytical Chemistry</i> , 2020, 92, 5379-5386.	6.5	4
215	Elevated colonic microbiota-associated paucimannosidic and truncated N-glycans in pediatric ulcerative colitis. <i>Journal of Proteomics</i> , 2021, 249, 104369.	2.4	4
216	Functionalizing poly(cyclic olefins) using copper-catalyzed azide-alkyne click reactions. <i>Canadian Journal of Chemistry</i> , 2011, 89, 608-615.	1.1	3

#	ARTICLE	IF	CITATIONS
217	Integrative Proteomics. <i>Proteomics</i> , 2013, 13, 1231-1232.	2.2	3
218	A simultaneous identification and quantification strategy for determination of sulfhydryl-containing metabolites in normal- and high-fat diet hamsters using stable isotope labeling combined with LC-MS. <i>Analytica Chimica Acta</i> , 2021, 1184, 339016.	5.4	3
219	Towards an Integrated Analytical Technology for the Generation of Multidimensional Protein Expression Maps. , 2000, , 143-162.		3
220	Comprehensive Assessment of Functional Effects of Commonly Used Sugar Substitute Sweeteners on <i>Ex Vivo</i> Human Gut Microbiome. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	3
221	The Achilles' heel of proteomics. <i>Trends in Biotechnology</i> , 2000, 18, 483.	9.3	2
222	Associations between Cellular Energy and Pediatric Inflammatory Bowel Disease Patient Response to Treatment. <i>Journal of Proteome Research</i> , 2021, 20, 4393-4404.	3.7	2
223	Predicting Glycerophosphoinositol Identities in Lipidomic Datasets Using VaLID (Visualization and) Tj ETQq1 1 0.784314 rgBT /Overlook 2014, 2014, 1-8.	1.9	1
224	Methods in Enzymology, Volumes 270 and 271, High-Resolution Separation and Analysis of Biological Macromolecules. Edited by Barry L. Karger and William S. Hancock. <i>Analytical Biochemistry</i> , 1997, 246, 268-269.	2.4	0
225	Large-scale screening on small scale. <i>Trends in Biotechnology</i> , 2000, 18, 363-364.	9.3	0
226	Web surfing in yeast: a network of proteins. <i>Trends in Biotechnology</i> , 2001, 19, 85-86.	9.3	0
227	Finding the "lost" genes. <i>Trends in Biotechnology</i> , 2002, 20, 144.	9.3	0
228	Mapping the switchboard of cellular biology by mass spectrometry. <i>Trends in Biotechnology</i> , 2002, 20, 234.	9.3	0
229	Single-cell genome expression analysis?. <i>Trends in Biotechnology</i> , 2002, 20, 449.	9.3	0
230	Protein Technologies: Two-Dimensional Gel Electrophoresis and Mass Spectrometry for Proteomic Studies: State-of-the-Art. , 0, , 225-252.		0
231	Phosphoproteomics in Drug Discovery and Development. , 2006, , 265-278.		0
232	Solid-Phase Extraction-Capillary Zone Electrophoresis-Mass Spectrometry Analysis of Low-Abundance Proteins. <i>Principles and Practice</i> , 2001, , 75-101.	0.3	0
233	The Use of ¹⁸ O Labeling as a Tool for Proteomic Applications. , 2003, , 145-179.		0
234	Identification of Chromatin-Binding Protein Complexes. , 2014, , 117-131.		0

#	ARTICLE	IF	CITATIONS
235	Proteomics: the basic overview. <i>Methods of Biochemical Analysis</i> , 2005, 45, 1-62.	0.2	0
236	Mapping protein-protein interactions. <i>Methods of Biochemical Analysis</i> , 2005, 45, 63-84.	0.2	0