

Daniel A Figeys

List of Publications by Year in descending order

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Version: 2024-02-01

236
papers

16,062
citations

25423

59
h-index

23173

116
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267
all docs

267
docs citations

267
times ranked

20485
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. <i>Cancer Cell</i> , 2022, 40, 70-87.e15.	7.7	120
2	Structural analysis of <i>Atopobium parvulum</i> SufS cysteine desulfurase linked to Crohn's disease. <i>FEBS Letters</i> , 2022, 596, 898-909.	1.3	5
3	Evaluating live microbiota biobanking using an <i>ex vivo</i> microbiome assay and metaproteomics. <i>Gut Microbes</i> , 2022, 14, 2035658.	4.3	7
4	iMetaLab Suite: A one-stop toolset for metaproteomics. , 2022, 1, .		7
5	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, .	1.2	3
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.	5.3	297
7	Identification of novel lipid droplet factors that regulate lipophagy and cholesterol efflux in macrophage foam cells. <i>Autophagy</i> , 2021, 17, 3671-3689.	4.3	90
8	Exploring the Microbiome-Wide Lysine Acetylation, Succinylation, and Propionylation in Human Gut Microbiota. <i>Analytical Chemistry</i> , 2021, 93, 6594-6598.	3.2	6
9	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.	3.9	159
10	Examining the Effects of an Anti-Salmonella Bacteriophage Preparation, BAFASAL [®] , on Ex-Vivo Human Gut Microbiome Composition and Function Using a Multi-Omics Approach. <i>Viruses</i> , 2021, 13, 1734.	1.5	5
11	Associations between Cellular Energy and Pediatric Inflammatory Bowel Disease Patient Response to Treatment. <i>Journal of Proteome Research</i> , 2021, 20, 4393-4404.	1.8	2
12	Elevated colonic microbiota-associated paucimannosidic and truncated N-glycans in pediatric ulcerative colitis. <i>Journal of Proteomics</i> , 2021, 249, 104369.	1.2	4
13	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.	2.6	3
14	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.	6.5	6
15	Chemoenzymatic Method for Glycoproteomic N-Glycan Type Quantitation. <i>Analytical Chemistry</i> , 2020, 92, 1618-1627.	3.2	11
16	Studying the Temporal Dynamics of the Gut Microbiota Using Metabolic Stable Isotope Labeling and Metaproteomics. <i>Analytical Chemistry</i> , 2020, 92, 15711-15718.	3.2	5
17	Widespread protein lysine acetylation in gut microbiome and its alterations in patients with Crohn's disease. <i>Nature Communications</i> , 2020, 11, 4120.	5.8	32
18	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.	2.7	10

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19	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.	1.9	15
20	pepFunk: a tool for peptide-centric functional analysis of metaproteomic human gut microbiome studies. <i>Bioinformatics</i> , 2020, 36, 4171-4179.	1.8	7
21	Berberine and its structural analogs have differing effects on functional profiles of individual gut microbiomes. <i>Gut Microbes</i> , 2020, 11, 1348-1361.	4.3	30
22	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.	1.2	21
23	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.	1.2	5
24	RapidAIM: a culture- and metaproteomics-based Rapid Assay of Individual Microbiome responses to drugs. <i>Microbiome</i> , 2020, 8, 33.	4.9	209
25	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.	2.5	13
26	Differential Lysis Approach Enables Selective Extraction of Taxon-Specific Proteins for Gut Metaproteomics. <i>Analytical Chemistry</i> , 2020, 92, 5379-5386.	3.2	4
27	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.	1.2	8
28	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.	1.2	7
29	Metaproteomic and Metabolomic Approaches for Characterizing the Gut Microbiome. <i>Proteomics</i> , 2019, 19, e1800363.	1.3	28
30	Therapeutic Targeting of Casein Kinase 1 β in an Alzheimer's Disease Mouse Model. <i>Journal of Proteome Research</i> , 2019, 18, 3383-3393.	1.8	25
31	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.	4.9	65
32	An in vitro model maintaining taxon-specific functional activities of the gut microbiome. <i>Nature Communications</i> , 2019, 10, 4146.	5.8	70
33	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.	1.9	17
34	Perspective and Guidelines for Metaproteomics in Microbiome Studies. <i>Journal of Proteome Research</i> , 2019, 18, 2370-2380.	1.8	63
35	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.	2.1	37
36	Advancing functional and translational microbiome research using meta-omics approaches. <i>Microbiome</i> , 2019, 7, 154.	4.9	177

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37	Aging Disrupts the Circadian Patterns of Protein Expression in the Murine Hippocampus. <i>Frontiers in Aging Neuroscience</i> , 2019, 11, 368.	1.7	25
38	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.	1.2	7
39	Open: Mucosal-luminal interface proteomics reveals biomarkers of pediatric inflammatory bowel disease-associated colitis. <i>American Journal of Gastroenterology</i> , 2018, 113, 713-724.	0.2	23
40	Assessing the impact of protein extraction methods for human gut metaproteomics. <i>Journal of Proteomics</i> , 2018, 180, 120-127.	1.2	115
41	Proteomic and Metaproteomic Approaches to Understand Host-Microbe Interactions. <i>Analytical Chemistry</i> , 2018, 90, 86-109.	3.2	44
42	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.	1.8	41
43	Separation and characterization of human microbiomes by metaproteomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2018, 108, 221-230.	5.8	4
44	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.	1.8	14
45	Metaproteomics reveals associations between microbiome and intestinal extracellular vesicle proteins in pediatric inflammatory bowel disease. <i>Nature Communications</i> , 2018, 9, 2873.	5.8	209
46	iMetaLab 1.0: a web platform for metaproteomics data analysis. <i>Bioinformatics</i> , 2018, 34, 3954-3956.	1.8	64
47	miR-132/212 Modulates Seasonal Adaptation and Dendritic Morphology of the Central Circadian Clock. <i>Cell Reports</i> , 2017, 19, 505-520.	2.9	45
48	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.	1.6	17
49	Deep Metaproteomics Approach for the Study of Human Microbiomes. <i>Analytical Chemistry</i> , 2017, 89, 9407-9415.	3.2	83
50	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.	6.1	69
51	PINK1-mediated phosphorylation of LETM1 regulates mitochondrial calcium transport and protects neurons against mitochondrial stress. <i>Nature Communications</i> , 2017, 8, 1399.	5.8	87
52	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.	1.2	26
53	Phosphoproteome Profiling Reveals Circadian Clock Regulation of Posttranslational Modifications in the Murine Hippocampus. <i>Frontiers in Neurology</i> , 2017, 8, 110.	1.1	35
54	MetaLab: an automated pipeline for metaproteomic data analysis. <i>Microbiome</i> , 2017, 5, 157.	4.9	128

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55	Metabolic Reprogramming by Hexosamine Biosynthetic and Golgi N-Glycan Branching Pathways. <i>Scientific Reports</i> , 2016, 6, 23043.	1.6	84
56	Proteomic analysis of minute amount of colonic biopsies by enteroscopy sampling. <i>Biochemical and Biophysical Research Communications</i> , 2016, 476, 286-292.	1.0	20
57	Proteome profiling reveals regional protein alteration in cerebrum of common marmoset (<i>Callithrix</i>) Tj ETQq1 1 0.784314 rgBT /Overlaid	2.0	11
58	Detergent-Assisted Glycoprotein Capture: A Versatile Tool for In-Depth N-Glycoproteome Analysis. <i>Journal of Proteome Research</i> , 2016, 15, 2080-2086.	1.8	13
59	Altered intestinal microbiotaâ€‘host mitochondria crosstalk in new onset Crohnâ€™s disease. <i>Nature Communications</i> , 2016, 7, 13419.	5.8	326
60	N-Glycopeptide Reduction with Exoglycosidases Enables Accurate Characterization of Site-Specific N-Glycosylation. <i>Analytical Chemistry</i> , 2016, 88, 11837-11843.	3.2	14
61	<i>In Vitro</i> Metabolic Labeling of Intestinal Microbiota for Quantitative Metaproteomics. <i>Analytical Chemistry</i> , 2016, 88, 6120-6125.	3.2	40
62	MetaPro-IQ: a universal metaproteomic approach to studying human and mouse gut microbiota. <i>Microbiome</i> , 2016, 4, 31.	4.9	154
63	Peptide-Centric Approaches Provide an Alternative Perspective To Re-Examine Quantitative Proteomic Data. <i>Analytical Chemistry</i> , 2016, 88, 1973-1978.	3.2	14
64	Bottom-Up Proteomics (2013â€‘2015): Keeping up in the Era of Systems Biology. <i>Analytical Chemistry</i> , 2016, 88, 95-121.	3.2	52
65	Quantitative proteomic analysis of <i>Dunaliella salina</i> upon acute arsenate exposure. <i>Chemosphere</i> , 2016, 145, 112-118.	4.2	31
66	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.	3.2	12
67	A charge-suppressing strategy for probing protein methylation. <i>Chemical Communications</i> , 2016, 52, 5474-5477.	2.2	30
68	17â€‘Estradiol results in a proprotein convertase subtilisin/kexin type 9â€‘dependent increase in lowâ€‘density lipoprotein receptor levels in human hepatic HuH7 cells. <i>FEBS Journal</i> , 2015, 282, 2682-2696.	2.2	14
69	Methylmercury can induce Parkinsonâ€™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.	0.7	28
70	Activityâ€‘based profiling of the proteasome pathway during hepatitis C virus infection. <i>Proteomics</i> , 2015, 15, 3815-3825.	1.3	6
71	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.	1.0	13
72	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.	1.6	52

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73	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.	2.9	17
74	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.	1.4	69
75	Discovery of Substrates for a SET Domain Lysine Methyltransferase Predicted by Multistate Computational Protein Design. <i>Structure</i> , 2015, 23, 206-215.	1.6	34
76	Proteomic Analysis of Cerebellum in Common Marmoset Exposed to Methylmercury. <i>Toxicological Sciences</i> , 2015, 146, 43-51.	1.4	14
77	Quantitative site-specific ADP-ribosylation profiling of DNA-dependent PARPs. <i>DNA Repair</i> , 2015, 30, 68-79.	1.3	56
78	MFG-E8 Is Critical for Embryonic Stem Cell-Mediated T Cell Immunomodulation. <i>Stem Cell Reports</i> , 2015, 5, 741-752.	2.3	17
79	Profiling Kinase Activity during Hepatitis C Virus Replication Using a Wortmannin Probe. <i>ACS Infectious Diseases</i> , 2015, 1, 443-452.	1.8	7
80	β -Catenin and NF- κ B co-activation triggered by TLR3 stimulation facilitates stem cell-like phenotypes in breast cancer. <i>Cell Death and Differentiation</i> , 2015, 22, 298-310.	5.0	87
81	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.	1.1	10
82	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.	1.1	42
83	Detecting Protein-Protein Interactions/Complex Components Using Mass Spectrometry Coupled Techniques. <i>Methods in Molecular Biology</i> , 2014, 1164, 1-13.	0.4	9
84	The Proteomic Landscape of the Suprachiasmatic Nucleus Clock Reveals Large-Scale Coordination of Key Biological Processes. <i>PLoS Genetics</i> , 2014, 10, e1004695.	1.5	63
85	Predicting Glycerophosphoinositol Identities in Lipidomic Datasets Using VaLID (Visualization and) Tj ETQq1 1 0.784314 rgBT /Overlo 2014, 2014, 1-8.	0.9	1
86	Regulation of the VHL/HIF-1 Pathway by DJ-1. <i>Journal of Neuroscience</i> , 2014, 34, 8043-8050.	1.7	34
87	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.	1.2	40
88	The functional diversity of protein lysine methylation. <i>Molecular Systems Biology</i> , 2014, 10, 724.	3.2	202
89	Fine Tuning of Proteomic Technologies to Improve Biological Findings: Advancements in 2011-2013. <i>Analytical Chemistry</i> , 2014, 86, 176-195.	3.2	18
90	Gelsolin regulates cisplatin sensitivity in human head-and-neck cancer. <i>International Journal of Cancer</i> , 2014, 135, 2760-2769.	2.3	28

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91	Large-scale characterization of intact N-glycopeptides using an automated glycoproteomic method. <i>Journal of Proteomics</i> , 2014, 110, 145-154.	1.2	57
92	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.	3.1	8
93	APols-Aided Protein Precipitation: A Rapid Method for Concentrating Proteins for Proteomic Analysis. <i>Journal of Membrane Biology</i> , 2014, 247, 941-947.	1.0	17
94	A New Chemical Probe for Phosphatidylinositol Kinase Activity. <i>ChemBioChem</i> , 2014, 15, 1253-1256.	1.3	25
95	Identification of Chromatin-Binding Protein Complexes. , 2014, , 117-131.		0
96	The Liver Connexin32 Interactome Is a Novel Plasma Membrane-Mitochondrial Signaling Nexus. <i>Journal of Proteome Research</i> , 2013, 12, 2597-2610.	1.8	45
97	Targeted lipidomics " advances in profiling lysophosphocholine and platelet-activating factor second messengers. <i>FEBS Journal</i> , 2013, 280, 5652-5667.	2.2	38
98	Myosin Phosphatase Modulates the Cardiac Cell Fate by Regulating the Subcellular Localization of Nkx2.5 in a Wnt/Rho-Associated Protein Kinase-Dependent Pathway. <i>Circulation Research</i> , 2013, 112, 257-266.	2.0	13
99	Analysis of human serum phosphopeptidome by a focused database searching strategy. <i>Journal of Proteomics</i> , 2013, 78, 389-397.	1.2	10
100	Phosphoproteome analysis of an early onset mouse model (TgCRND8) of Alzheimer's disease reveals temporal changes in neuronal and glia signaling pathways. <i>Proteomics</i> , 2013, 13, 1292-1305.	1.3	17
101	From Cells to Peptides: "One-Stop" Integrated Proteomic Processing Using Amphipols. <i>Journal of Proteome Research</i> , 2013, 12, 1512-1519.	1.8	28
102	Using neurolipidomics to identify phospholipid mediators of synaptic (dys)function in Alzheimer's Disease. <i>Frontiers in Physiology</i> , 2013, 4, 168.	1.3	60
103	Microsome-associated luminal lipid droplets in the regulation of lipoprotein secretion. <i>Current Opinion in Lipidology</i> , 2013, 24, 160-170.	1.2	33
104	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.	1.8	12
105	Integrative Proteomics. <i>Proteomics</i> , 2013, 13, 1231-1232.	1.3	3
106	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.	3.3	38
107	Combination of online enzyme digestion with stable isotope labeling for high-throughput quantitative proteome analysis. <i>Proteomics</i> , 2012, 12, 3129-3137.	1.3	14
108	Exploring the Yeast Acetylome Using Functional Genomics. <i>Cell</i> , 2012, 149, 936-948.	13.5	63

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109	A novel whole-cell lysate kinase assay identifies substrates of the p38 MAPK in differentiating myoblasts. <i>Skeletal Muscle</i> , 2012, 2, 5.	1.9	43
110	Advancements in Top-Down Proteomics. <i>Analytical Chemistry</i> , 2012, 84, 720-734.	3.2	80
111	Development of a Multiplexed Microfluidic Proteomic Reactor and Its Application for Studying Protein-Protein Interactions. <i>Analytical Chemistry</i> , 2011, 83, 4095-4102.	3.2	34
112	Quantitative Proteomic Analysis of PCSK9 Gain of Function in Human Hepatic HuH7 Cells. <i>Journal of Proteome Research</i> , 2011, 10, 2011-2026.	1.8	15
113	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.	3.2	57
114	Analytical Aspects of Proteomics: 2009-2010. <i>Analytical Chemistry</i> , 2011, 83, 4407-4426.	3.2	28
115	Functionalizing poly(cyclic olefins) using copper-catalyzed azide-alkyne click reactions. <i>Canadian Journal of Chemistry</i> , 2011, 89, 608-615.	0.6	3
116	Regulation of Septin Dynamics by the <i>Saccharomyces cerevisiae</i> Lysine Acetyltransferase NuA4. <i>PLoS ONE</i> , 2011, 6, e25336.	1.1	33
117	Proteomic reactors and their applications in biology. <i>FEBS Journal</i> , 2011, 278, 3796-3806.	2.2	33
118	Skeletal myosin light chain kinase regulates skeletal myogenesis by phosphorylation of MEF2C. <i>EMBO Journal</i> , 2011, 30, 2477-2489.	3.5	35
119	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.	1.8	16
120	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.	1.4	8
121	An enhanced chemically defined SILAC culture system for quantitative proteomics study of human embryonic stem cells. <i>Proteomics</i> , 2011, 11, 4040-4046.	1.3	9
122	Lysoform fragment ions facilitate the determination of stereospecificity of diacyl glycerophospholipids. <i>Rapid Communications in Mass Spectrometry</i> , 2011, 25, 205-217.	0.7	31
123	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.	1.5	103
124	Restriction of histone gene transcription to S phase by phosphorylation of a chromatin boundary protein. <i>Genes and Development</i> , 2011, 25, 2489-2501.	2.7	40
125	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.	2.5	31
126	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.	2.5	52

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127	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.	2.5	26
128	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.	1.6	91
129	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.	1.5	12
130	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.	1.1	14
131	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.	1.9	10
132	The tryptophan-rich domain of puroindoline 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.	1.8	35
133	Lipidomics era: Accomplishments and challenges. <i>Mass Spectrometry Reviews</i> , 2010, 29, 877-929.	2.8	161
134	Functional analysis of the missense APOC3 mutation Ala23Thr associated with human hypotriglyceridemia. <i>Journal of Lipid Research</i> , 2010, 51, 1524-1534.	2.0	53
135	Defining the budding yeast chromatin-associated interactome. <i>Molecular Systems Biology</i> , 2010, 6, 448.	3.2	58
136	Phospholipase C Activity Affinity Purifies with the Torpedo Nicotinic Acetylcholine Receptor. <i>Journal of Biological Chemistry</i> , 2010, 285, 10337-10343.	1.6	13
137	Nonsynonymous Mutations within APOB in Human Familial Hypobetalipoproteinemia. <i>Journal of Biological Chemistry</i> , 2010, 285, 6453-6464.	1.6	58
138	Analysis of the Subcellular Phosphoproteome Using a Novel Phosphoproteomic Reactor. <i>Journal of Proteome Research</i> , 2010, 9, 1279-1288.	1.8	25
139	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.	1.2	51
140	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.	0.5	12
141	Analysis of low-abundance proteins using the proteomic reactor with pH fractionation. <i>Talanta</i> , 2010, 80, 1526-1531.	2.9	16
142	Of proteins and DNA-proteomic role in the field of chromatin research. <i>Molecular BioSystems</i> , 2010, 6, 30-37.	2.9	4
143	A Novel Proteomics Approach for the Discovery of Chromatin-associated Protein Networks. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 870-882.	2.5	95
144	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.	3.3	64

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145	Proteomics: From Technology Developments to Biological Applications. <i>Analytical Chemistry</i> , 2009, 81, 4585-4599.	3.2	42
146	Glycoproteomic Reactor for Human Plasma. <i>Journal of Proteome Research</i> , 2009, 8, 556-566.	1.8	29
147	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.	2.0	9
148	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.	4.5	88
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