

Gary E Siuzdak

List of Publications by Year in descending order

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201
papers

33,937
citations

7069

78
h-index

3815

178
g-index

213
all docs

213
docs citations

213
times ranked

37491
citing authors

#	ARTICLE	IF	CITATIONS
1	XCMS: Processing Mass Spectrometry Data for Metabolite Profiling Using Nonlinear Peak Alignment, Matching, and Identification. <i>Analytical Chemistry</i> , 2006, 78, 779-787.	3.2	4,128
2	Metabolomics analysis reveals large effects of gut microflora on mammalian blood metabolites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3698-3703.	3.3	2,198
3	METLIN. <i>Therapeutic Drug Monitoring</i> , 2005, 27, 747-751.	1.0	1,960
4	Metabolomics: the apogee of the omics trilogy. <i>Nature Reviews Molecular Cell Biology</i> , 2012, 13, 263-269.	16.1	1,931
5	Metabolomics: beyond biomarkers and towards mechanisms. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 451-459.	16.1	1,723
6	Generation of Induced Pluripotent Stem Cells Using Recombinant Proteins. <i>Cell Stem Cell</i> , 2009, 4, 381-384.	5.2	1,652
7	XCMS Online: A Web-Based Platform to Process Untargeted Metabolomic Data. <i>Analytical Chemistry</i> , 2012, 84, 5035-5039.	3.2	1,087
8	Desorption/ionization mass spectrometry on porous silicon. <i>Nature</i> , 1999, 399, 243-246.	13.7	1,046
9	METLIN: A Technology Platform for Identifying Knowns and Unknowns. <i>Analytical Chemistry</i> , 2018, 90, 3156-3164.	3.2	696
10	Identification of bioactive metabolites using activity metabolomics. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 353-367.	16.1	602
11	An accelerated workflow for untargeted metabolomics using the METLIN database. <i>Nature Biotechnology</i> , 2012, 30, 826-828.	9.4	472
12	Clathrate nanostructures for mass spectrometry. <i>Nature</i> , 2007, 449, 1033-1036.	13.7	457
13	Metabolic oxidation regulates embryonic stem cell differentiation. <i>Nature Chemical Biology</i> , 2010, 6, 411-417.	3.9	454
14	The metabolome of induced pluripotent stem cells reveals metabolic changes occurring in somatic cell reprogramming. <i>Cell Research</i> , 2012, 22, 168-177.	5.7	452
15	Solvent-Dependent Metabolite Distribution, Clustering, and Protein Extraction for Serum Profiling with Mass Spectrometry. <i>Analytical Chemistry</i> , 2006, 78, 743-752.	3.2	414
16	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756.	9.0	403
17	Liquid chromatography quadrupole time-of-flight mass spectrometry characterization of metabolites guided by the METLIN database. <i>Nature Protocols</i> , 2013, 8, 451-460.	5.5	379
18	Porous Silicon as a Versatile Platform for Laser Desorption/Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2001, 73, 612-619.	3.2	337

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19	Interactive XCMS Online: Simplifying Advanced Metabolomic Data Processing and Subsequent Statistical Analyses. <i>Analytical Chemistry</i> , 2014, 86, 6931-6939.	3.2	332
20	Microbial metalloproteomes are largely uncharacterized. <i>Nature</i> , 2010, 466, 779-782.	13.7	330
21	Metabolomics activity screening for identifying metabolites that modulate phenotype. <i>Nature Biotechnology</i> , 2018, 36, 316-320.	9.4	319
22	Assignment of Endogenous Substrates to Enzymes by Global Metabolite Profiling. <i>Biochemistry</i> , 2004, 43, 14332-14339.	1.2	302
23	Metabolism Links Bacterial Biofilms and Colon Carcinogenesis. <i>Cell Metabolism</i> , 2015, 21, 891-897.	7.2	288
24	Nonlinear Data Alignment for UPLC-MS and HPLC-MS Based Metabolomics: Quantitative Analysis of Endogenous and Exogenous Metabolites in Human Serum. <i>Analytical Chemistry</i> , 2006, 78, 3289-3295.	3.2	267
25	From Exogenous to Endogenous: The Inevitable Imprint of Mass Spectrometry in Metabolomics. <i>Journal of Proteome Research</i> , 2007, 6, 459-468.	1.8	254
26	Toward Omic Scale Metabolite Profiling: A Dual Separation-Mass Spectrometry Approach for Coverage of Lipid and Central Carbon Metabolism. <i>Analytical Chemistry</i> , 2013, 85, 6876-6884.	3.2	242
27	An assembly landscape for the 30S ribosomal subunit. <i>Nature</i> , 2005, 438, 628-632.	13.7	238
28	Expanding Coverage of the Metabolome for Global Metabolite Profiling. <i>Analytical Chemistry</i> , 2011, 83, 2152-2161.	3.2	233
29	High Sensitivity and Analyte Capture with Desorption/Ionization Mass Spectrometry on Silylated Porous Silicon. <i>Analytical Chemistry</i> , 2004, 76, 4484-4489.	3.2	223
30	Data processing, multi-omic pathway mapping, and metabolite activity analysis using XCMS Online. <i>Nature Protocols</i> , 2018, 13, 633-651.	5.5	207
31	Multiple organic anion transporters contribute to net renal excretion of uric acid. <i>Physiological Genomics</i> , 2008, 33, 180-192.	1.0	203
32	The Expanding Role of Mass Spectrometry in Metabolite Profiling and Characterization. <i>ChemBioChem</i> , 2005, 6, 1941-1951.	1.3	198
33	Investigating Molecular Recognition by Mass Spectrometry: Characterization of Calixarene-Based Self-Assembling Capsule Hosts with Charged Guests. <i>Journal of the American Chemical Society</i> , 1999, 121, 4568-4579.	6.6	184
34	Desorption/ionization on silicon (DIOS) mass spectrometry: background and applications. <i>International Journal of Mass Spectrometry</i> , 2003, 226, 107-116.	0.7	183
35	Metabolomics implicates altered sphingolipids in chronic pain of neuropathic origin. <i>Nature Chemical Biology</i> , 2012, 8, 232-234.	3.9	183
36	Multiple Ionization Mass Spectrometry Strategy Used To Reveal the Complexity of Metabolomics. <i>Analytical Chemistry</i> , 2008, 80, 421-429.	3.2	182

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37	Evidence of Viral Capsid Dynamics Using Limited Proteolysis and Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 1998, 273, 673-676.	1.6	170
38	Systems biology guided by XCMS Online metabolomics. <i>Nature Methods</i> , 2017, 14, 461-462.	9.0	168
39	ABHD12 controls brain lysophosphatidylserine pathways that are deregulated in a murine model of the neurodegenerative disease PHARC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1500-1505.	3.3	163
40	Endothelial Targeting of Cowpea Mosaic Virus (CPMV) via Surface Vimentin. <i>PLoS Pathogens</i> , 2009, 5, e1000417.	2.1	160
41	Hypoxia-induced metabolic stress in retinal pigment epithelial cells is sufficient to induce photoreceptor degeneration. <i>ELife</i> , 2016, 5, .	2.8	159
42	Autonomous Metabolomics for Rapid Metabolite Identification in Global Profiling. <i>Analytical Chemistry</i> , 2015, 87, 884-891.	3.2	157
43	Meta-analysis of untargeted metabolomic data from multiple profiling experiments. <i>Nature Protocols</i> , 2012, 7, 508-516.	5.5	154
44	Membrane Cofactor Protein Is a Receptor for Adenoviruses Associated with Epidemic Keratoconjunctivitis. <i>Journal of Virology</i> , 2004, 78, 3897-3905.	1.5	153
45	Metabolomics Identifies Perturbations in Human Disorders of Propionate Metabolism. <i>Clinical Chemistry</i> , 2007, 53, 2169-2176.	1.5	148
46	Nanostructure-Initiator Mass Spectrometry Metabolite Analysis and Imaging. <i>Analytical Chemistry</i> , 2011, 83, 2-7.	3.2	142
47	A nanostructure-initiator mass spectrometry-based enzyme activity assay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3678-3683.	3.3	138
48	Variability Analysis of Human Plasma and Cerebral Spinal Fluid Reveals Statistical Significance of Changes in Mass Spectrometry-Based Metabolomics Data. <i>Analytical Chemistry</i> , 2009, 81, 8538-8544.	3.2	128
49	Annotation: A Computational Solution for Streamlining Metabolomics Analysis. <i>Analytical Chemistry</i> , 2018, 90, 480-489.	3.2	126
50	Metabolomic analysis of the cerebrospinal fluid reveals changes in phospholipase expression in the CNS of SIV-infected macaques. <i>Journal of Clinical Investigation</i> , 2008, 118, 2661-9.	3.9	125
51	Chemoenzymatic Preparation of Novel Cyclic Imine Sugars and Rapid Biological Activity Evaluation Using Electrospray Mass Spectrometry and Kinetic Analysis. <i>Journal of the American Chemical Society</i> , 1997, 119, 8146-8151.	6.6	123
52	Nanostructure-initiator mass spectrometry: a protocol for preparing and applying NIMS surfaces for high-sensitivity mass analysis. <i>Nature Protocols</i> , 2008, 3, 1341-1349.	5.5	122
53	The Structure of Apo Human Glutamate Dehydrogenase Details Subunit Communication and Allostery. <i>Journal of Molecular Biology</i> , 2002, 318, 765-777.	2.0	119
54	Nanostructure Initiator Mass Spectrometry: Tissue Imaging and Direct Biofluid Analysis. <i>Analytical Chemistry</i> , 2009, 81, 2969-2975.	3.2	117

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55	Maintaining retinal astrocytes normalizes revascularization and prevents vascular pathology associated with oxygen-induced retinopathy. <i>Glia</i> , 2010, 58, 43-54.	2.5	116
56	Antioxidant or neurotrophic factor treatment preserves function in a mouse model of neovascularization-associated oxidative stress. <i>Journal of Clinical Investigation</i> , 2009, 119, 611-623.	3.9	114
57	The METLIN small molecule dataset for machine learning-based retention time prediction. <i>Nature Communications</i> , 2019, 10, 5811.	5.8	114
58	Thermal Degradation of Small Molecules: A Global Metabolomic Investigation. <i>Analytical Chemistry</i> , 2015, 87, 10935-10941.	3.2	112
59	Bioinformatics: The Next Frontier of Metabolomics. <i>Analytical Chemistry</i> , 2015, 87, 147-156.	3.2	112
60	XCMS-MRM and METLIN-MRM: a cloud library and public resource for targeted analysis of small molecules. <i>Nature Methods</i> , 2018, 15, 681-684.	9.0	112
61	Monitoring Enzyme Catalysis with Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2000, 275, 13455-13459.	1.6	110
62	Exposome-Scale Investigations Guided by Global Metabolomics, Pathway Analysis, and Cognitive Computing. <i>Analytical Chemistry</i> , 2017, 89, 11505-11513.	3.2	106
63	Spontaneous DNA damage to the nuclear genome promotes senescence, redox imbalance and aging. <i>Redox Biology</i> , 2018, 17, 259-273.	3.9	103
64	METLIN MS2 molecular standards database: a broad chemical and biological resource. <i>Nature Methods</i> , 2020, 17, 953-954.	9.0	102
65	Evaluation of the safety and immunomodulatory effects of sargramostim in a randomized, double-blind phase 1 clinical Parkinson's disease trial. <i>Npj Parkinson's Disease</i> , 2017, 3, 10.	2.5	98
66	PGRMC2 is an intracellular haem chaperone critical for adipocyte function. <i>Nature</i> , 2019, 576, 138-142.	13.7	96
67	metaXCMS: Second-Order Analysis of Untargeted Metabolomics Data. <i>Analytical Chemistry</i> , 2011, 83, 696-700.	3.2	95
68	Detection of Carbohydrates and Steroids by Cation-Enhanced Nanostructure-Initiator Mass Spectrometry (NIMS) for Biofluid Analysis and Tissue Imaging. <i>Analytical Chemistry</i> , 2010, 82, 121-128.	3.2	94
69	Quench-flow experiments combined with mass spectrometry show apomyoglobin folds through an obligatory intermediate. <i>Protein Science</i> , 1999, 8, 45-49.	3.1	93
70	Metabolic drift in the aging brain. <i>Aging</i> , 2016, 8, 1000-1020.	1.4	89
71	Desorption-ionization on silicon mass spectrometry: an application in forensics. <i>Analytica Chimica Acta</i> , 2001, 442, 183-190.	2.6	87
72	Crystallographically identical virus capsids display different properties in solution. <i>Nature Structural Biology</i> , 1999, 6, 114-116.	9.7	86

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73	A View from Above: Cloud Plots to Visualize Global Metabolomic Data. <i>Analytical Chemistry</i> , 2013, 85, 798-804.	3.2	85
74	Metabolite and Microbiome Interplay in Cancer Immunotherapy. <i>Cancer Research</i> , 2016, 76, 6146-6152.	0.4	85
75	Generation of Retinal Pigment Epithelial Cells from Small Molecules and <i>OCT4</i> Reprogrammed Human Induced Pluripotent Stem Cells. <i>Stem Cells Translational Medicine</i> , 2012, 1, 96-109.	1.6	83
76	A fiber-deprived diet disturbs the fine-scale spatial architecture of the murine colon microbiome. <i>Nature Communications</i> , 2019, 10, 4366.	5.8	82
77	Selective Metabolite and Peptide Capture/Mass Detection Using Fluorous Affinity Tags. <i>Journal of Proteome Research</i> , 2007, 6, 1492-1499.	1.8	81
78	Direct characterization of solid phase resin-bound molecules by mass spectrometry. <i>Bioorganic and Medicinal Chemistry Letters</i> , 1996, 6, 979-982.	1.0	80
79	Global metabolomics reveals metabolic dysregulation in ischemic retinopathy. <i>Metabolomics</i> , 2016, 12, 15.	1.4	80
80	Electrospray ion mobility spectrometry of intact viruses. <i>Spectroscopy</i> , 2004, 18, 31-36.	0.8	79
81	Metabolomics-based discovery of a metabolite that enhances oligodendrocyte maturation. <i>Nature Chemical Biology</i> , 2018, 14, 22-28.	3.9	79
82	Nanoelectrospray Mass Spectrometry and Precursor Ion Monitoring for Quantitative Steroid Analysis and Attomole Sensitivity. <i>Analytical Chemistry</i> , 1999, 71, 2358-2363.	3.2	78
83	Intestinal bitter taste receptor activation alters hormone secretion and imparts metabolic benefits. <i>Molecular Metabolism</i> , 2018, 16, 76-87.	3.0	78
84	Differential Macrophage Polarization Promotes Tissue Remodeling and Repair in a Model of Ischemic Retinopathy. <i>Scientific Reports</i> , 2011, 1, 76.	1.6	77
85	Surface Modification and Laser Pulse Length Effects on Internal Energy Transfer in DIOS. <i>Journal of Physical Chemistry B</i> , 2005, 109, 24450-24456.	1.2	76
86	Autonomous METLIN-Guided In-source Fragment Annotation for Untargeted Metabolomics. <i>Analytical Chemistry</i> , 2019, 91, 3246-3253.	3.2	76
87	Desorption/Ionization on Silicon Time-of-Flight/Time-of-Flight Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 2504-2506.	3.2	74
88	High surface area of porous silicon drives desorption of intact molecules. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 1945-1949.	1.2	74
89	Organic Anion Transporter 3 Contributes to the Regulation of Blood Pressure. <i>Journal of the American Society of Nephrology: JASN</i> , 2008, 19, 1732-1740.	3.0	72
90	Electrospray Ionization of a Whole Virus: Analyzing Mass, Structure, and Viability. <i>ChemBioChem</i> , 2004, 5, 258-260.	1.3	70

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91	Mass Spectrometry in Viral Proteomics. <i>Accounts of Chemical Research</i> , 2000, 33, 179-187.	7.6	68
92	Human rhinovirus capsid dynamics is controlled by canyon flexibility. <i>Virology</i> , 2003, 314, 34-44.	1.1	66
93	Correlating the Transcriptome, Proteome, and Metabolome in the Environmental Adaptation of a Hyperthermophile. <i>Journal of Proteome Research</i> , 2008, 7, 1027-1035.	1.8	66
94	Brain Region Mapping Using Global Metabolomics. <i>Chemistry and Biology</i> , 2014, 21, 1575-1584.	6.2	65
95	Probing Protein/Protein Interactions with Mass Spectrometry and Isotopic Labeling: A Analysis of the p21/Cdk2 Complex. <i>Journal of the American Chemical Society</i> , 1996, 118, 5320-5321.	6.6	62
96	A Mass Spectrometry Plate Reader: Monitoring Enzyme Activity and Inhibition with a Desorption/Ionization on Silicon (DIOS) Platform. <i>ChemBioChem</i> , 2004, 5, 921-927.	1.3	62
97	Arteriovenous Blood Metabolomics: A Readout of Intra-Tissue Metabostasis. <i>Scientific Reports</i> , 2015, 5, 12757.	1.6	62
98	New Catalysts for the Asymmetric Hydrosilylation of Ketones Discovered by Mass Spectrometry Screening. <i>Journal of Organic Chemistry</i> , 2003, 68, 2540-2546.	1.7	61
99	Reactivity-Based One-Pot Synthesis of the Tumor-Associated Antigen N3 Minor Octasaccharide for the Development of a Photocleavable DIOS-MS Sugar Array. <i>Angewandte Chemie - International Edition</i> , 2006, 45, 2753-2757.	7.2	61
100	METLIN: A Tandem Mass Spectral Library of Standards. <i>Methods in Molecular Biology</i> , 2020, 2104, 149-163.	0.4	61
101	Molecular Basis for the Specificity of p27 Toward Cyclin-dependent Kinases that Regulate Cell Division. <i>Journal of Molecular Biology</i> , 2005, 349, 764-773.	2.0	60
102	Metabolomics annotates ABHD3 as a physiologic regulator of medium-chain phospholipids. <i>Nature Chemical Biology</i> , 2011, 7, 763-765.	3.9	59
103	Probing protein structure using biochemical and biophysical methods. <i>Journal of Chromatography A</i> , 1997, 777, 23-30.	1.8	58
104	Quantitative Analysis with Desorption/Ionization on Silicon Mass Spectrometry Using Electrospray Deposition. <i>Analytical Chemistry</i> , 2003, 75, 5475-5479.	3.2	58
105	Sepsis Plasma Protein Profiling with Immunodepletion, Three-Dimensional Liquid Chromatography Tandem Mass Spectrometry, and Spectrum Counting. <i>Journal of Proteome Research</i> , 2006, 5, 3154-3160.	1.8	58
106	Combined Immunocapture and Laser Desorption/Ionization Mass Spectrometry on Porous Silicon. <i>Analytical Chemistry</i> , 2010, 82, 4201-4208.	3.2	58
107	Probing viruses with mass spectrometry. , 1998, 33, 203-211.		57
108	Affinity mass spectrometry from a tailored porous silicon surface Electronic supplementary information (ESI) available: synthesis and characterization of new compounds, experimental details. See http://www.rsc.org/suppdata/cc/b4/b408200a/ . <i>Chemical Communications</i> , 2004, , 2108.	2.2	56

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109	Selective inhibition of Î²-1,4- and Î±-1,3-galactosyltransferases: donor sugar-nucleotide based approach. <i>Bioorganic and Medicinal Chemistry</i> , 1999, 7, 401-409.	1.4	55
110	Surfactant-Enhanced Desorption/Ionization on Silicon Mass Spectrometry. <i>Analytical Chemistry</i> , 2006, 78, 272-278.	3.2	52
111	Metabolomics Reveals that Dietary Xenoestrogens Alter Cellular Metabolism Induced by Palbociclib/Letrozole Combination Cancer Therapy. <i>Cell Chemical Biology</i> , 2018, 25, 291-300.e3.	2.5	52
112	Peptide and protein analysis with mass spectrometry. <i>Spectroscopy</i> , 2002, 16, 15-28.	0.8	50
113	Comprehensive bioimaging with fluorinated nanoparticles using breathable liquids. <i>Nature Communications</i> , 2015, 6, 5998.	5.8	50
114	Identification of a New Endogenous Metabolite and the Characterization of Its Protein Interactions through an Immobilization Approach. <i>Journal of the American Chemical Society</i> , 2009, 131, 378-386.	6.6	49
115	Acylcarnitines are anticoagulants that inhibit factor Xa and are reduced in venous thrombosis, based on metabolomics data. <i>Blood</i> , 2015, 126, 1595-1600.	0.6	49
116	An Automated MALDI Mass Spectrometry Approach for Optimizing Cyclosporin Extraction and Quantitation. <i>Analytical Chemistry</i> , 1997, 69, 3767-3771.	3.2	48
117	Structural Examination of Supramolecular Architectures by Electrospray Ionization Mass Spectrometry. <i>European Journal of Organic Chemistry</i> , 1999, 1999, 1325-1331.	1.2	48
118	Metabolomic data streaming for biology-dependent data acquisition. <i>Nature Biotechnology</i> , 2014, 32, 524-527.	9.4	45
119	Gas-Phase Micelles. <i>Angewandte Chemie International Edition in English</i> , 1995, 34, 2053-2055.	4.4	44
120	Monitoring metabolic responses to chemotherapy in single cells and tumors using nanostructure-initiator mass spectrometry (NIMS) imaging. <i>Cancer & Metabolism</i> , 2013, 1, 4.	2.4	43
121	Metabolomics Data Processing Using XCMS. <i>Methods in Molecular Biology</i> , 2020, 2104, 11-24.	0.4	43
122	Mass Spectrometry Reveals Specific and Global Molecular Transformations during Viral Infection. <i>Journal of Proteome Research</i> , 2006, 5, 2405-2416.	1.8	42
123	Enhanced in-Source Fragmentation Annotation Enables Novel Data Independent Acquisition and Autonomous METLIN Molecular Identification. <i>Analytical Chemistry</i> , 2020, 92, 6051-6059.	3.2	42
124	isoMETLIN: A Database for Isotope-Based Metabolomics. <i>Analytical Chemistry</i> , 2014, 86, 9358-9361.	3.2	41
125	Cleavable Linkers for Porous Silicon-Based Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2004, 43, 1255-1260.	7.2	40
126	Metabolic rewiring of the hypertensive kidney. <i>Science Signaling</i> , 2019, 12, .	1.6	40

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127	Novel Multiprotein Complexes Identified in the Hyperthermophilic Archaeon <i>Pyrococcus furiosus</i> by Non-denaturing Fractionation of the Native Proteome. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 735-751.	2.5	39
128	Generation of Induced Pluripotent Stem Cells Using Recombinant Proteins. <i>Cell Stem Cell</i> , 2009, 4, 581.	5.2	39
129	The Role of Metabolomics in Brain Metabolism Research. <i>Journal of NeuroImmune Pharmacology</i> , 2015, 10, 391-395.	2.1	39
130	An interactive cluster heat map to visualize and explore multidimensional metabolomic data. <i>Metabolomics</i> , 2015, 11, 1029-1034.	1.4	39
131	Identification of Modified Tryptophan Residues in Apolipoprotein B-100 Derived from Copper Ion-Oxidized Low-Density Lipoprotein. <i>Biochemistry</i> , 1999, 38, 15903-15908.	1.2	37
132	Fluorinated Gold Nanoparticles for Nanostructure Imaging Mass Spectrometry. <i>ACS Nano</i> , 2018, 12, 6938-6948.	7.3	37
133	High-Temperature Protein Mass Mapping Using a Thermophilic Protease. <i>Journal of the American Chemical Society</i> , 2001, 123, 1774-1775.	6.6	36
134	Maturation of a tetravirus capsid alters the dynamic properties and creates a metastable complex. <i>Virology</i> , 2005, 334, 17-27.	1.1	36
135	Metabolite discovery: Biochemistry's scientific driver. <i>Cell Metabolism</i> , 2022, 34, 21-34.	7.2	36
136	Liquid chromatography mass spectrometry of antisense oligonucleotides. <i>Bioorganic and Medicinal Chemistry Letters</i> , 1995, 5, 2863-2868.	1.0	34
137	The Glycerophospho Metabolome and Its Influence on Amino Acid Homeostasis Revealed by Brain Metabolomics of <i>GDE1</i> Mice. <i>Chemistry and Biology</i> , 2010, 17, 831-840.	6.2	34
138	Acoustic deposition with NIMS as a high-throughput enzyme activity assay. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 403, 707-711.	1.9	33
139	Response and Recovery in the Plasma Metabolome Tracks the Acute LCMV-Induced Immune Response. <i>Journal of Proteome Research</i> , 2009, 8, 3578-3587.	1.8	32
140	Cerebrospinal Fluid Proteomics Reveals Potential Pathogenic Changes in the Brains of SIV-Infected Monkeys. <i>Journal of Proteome Research</i> , 2009, 8, 2253-2260.	1.8	32
141	Quantitative Plasma Proteomic Profiling Identifies the Vitamin E Binding Protein Afamin as a Potential Pathogenic Factor in SIV Induced CNS Disease. <i>Journal of Proteome Research</i> , 2010, 9, 352-358.	1.8	32
142	Biomarkers for NeuroAIDS: The Widening Scope of Metabolomics. <i>Journal of NeuroImmune Pharmacology</i> , 2007, 2, 72-80.	2.1	31
143	Rice Tungro Bacilliform Virus Open Reading Frame 3 Encodes a Single 37-kDa Coat Protein. <i>Virology</i> , 1999, 253, 319-326.	1.1	30
144	Type I Signal Peptidase and Protein Secretion in <i>Staphylococcus epidermidis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 340-348.	1.0	29

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145	Metabolizing Data in the Cloud. Trends in Biotechnology, 2017, 35, 481-483.	4.9	29
146	Large scale physiological readjustment during growth enables rapid, comprehensive and inexpensive systems analysis. BMC Systems Biology, 2010, 4, 64.	3.0	27
147	Activation of Kappa Opioid Receptor Regulates the Hypothermic Response to Calorie Restriction and Limits Body Weight Loss. Current Biology, 2019, 29, 4291-4299.e4.	1.8	25
148	Phospholipid capture combined with non-linear chromatographic correction for improved serum metabolite profiling. Metabolomics, 2006, 2, 145-154.	1.4	24
149	Meta-analysis of global metabolomic data identifies metabolites associated with life-span extension. Metabolomics, 2014, 10, 737-743.	1.4	24
150	Autonomous Multimodal Metabolomics Data Integration for Comprehensive Pathway Analysis and Systems Biology. Analytical Chemistry, 2018, 90, 8396-8403.	3.2	24
151	Metabolic adaptation to calorie restriction. Science Signaling, 2020, 13, .	1.6	24
152	Phosphonium labeling for increasing metabolomic coverage of neutral lipids using electrospray ionization mass spectrometry. Rapid Communications in Mass Spectrometry, 2009, 23, 1849-1855.	0.7	23
153	Data Streaming for Metabolomics: Accelerating Data Processing and Analysis from Days to Minutes. Analytical Chemistry, 2017, 89, 1254-1259.	3.2	23
154	Quantitative ESI-TOF Analysis of Macromolecular Assembly Kinetics. Analytical Chemistry, 2008, 80, 9379-9386.	3.2	22
155	Coagulation and Complement Protein Differences Between Septic and Uninfected Systemic Inflammatory Response Syndrome Patients. Journal of Trauma, 2007, 62, 1082-1094.	2.3	20
156	A Computational Framework for Proteome-Wide Pursuit and Prediction of Metalloproteins using ICP-MS and MS/MS Data. BMC Bioinformatics, 2011, 12, 64.	1.2	20
157	Examination of the sialyl lewis X - calcium complex by electrospray mass spectrometry. Bioorganic and Medicinal Chemistry Letters, 1994, 4, 2863-2866.	1.0	19
158	Metabolomics activity screening of T cell α -induced colitis reveals anti-inflammatory metabolites. Science Signaling, 2021, 14, eabf6584.	1.6	19
159	Neutral Loss Mass Spectral Data Enhances Molecular Similarity Analysis in METLIN. Journal of the American Society for Mass Spectrometry, 2022, 33, 530-534.	1.2	19
160	Metabolomics relative quantitation with mass spectrometry using chemical derivatization and isotope labeling. Spectroscopy, 2008, 22, 327-343.	0.8	18
161	Discriminating precursors of common fragments for large-scale metabolite profiling by triple quadrupole mass spectrometry. Bioinformatics, 2015, 31, 2017-2023.	1.8	18
162	Morphology-Driven Control of Metabolite Selectivity Using Nanostructure-Initiator Mass Spectrometry. Analytical Chemistry, 2017, 89, 6521-6526.	3.2	18

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