

Joshua J Coon

List of Publications by Year in descending order

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284
papers

23,069
citations

10986

71
h-index

10734

138
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306
all docs

306
docs citations

306
times ranked

25584
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic and metabolomic profiling of acute and chronic stress events associated with military exercises. <i>Molecular Omics</i> , 2022, 18, 279-295.	2.8	4
2	Multi-omics analysis identifies essential regulators of mitochondrial stress response in two wild-type <i>C.Ælegans</i> strains. <i>IScience</i> , 2022, 25, 103734.	4.1	9
3	Tcof1 haploinsufficiency promotes early T cell precursor-like leukemia in <i>Nras</i> Q61R/+ mice. <i>Leukemia</i> , 2022, , .	7.2	0
4	Rapid Targeted Quantitation of Protein Overexpression with Direct Infusion Shotgun Proteome Analysis (DISPA-PRM). <i>Analytical Chemistry</i> , 2022, 94, 1965-1973.	6.5	8
5	Maximizing MS/MS Acquisition for Lipidomics Using Capillary Separation and Orbitrap Tribrid Mass Spectrometer. <i>Analytical Chemistry</i> , 2022, 94, 3394-3399.	6.5	9
6	Infrared Photoactivation Boosts Reporter Ion Yield in Isobaric Tagging. <i>Analytical Chemistry</i> , 2022, , .	6.5	2
7	High-Throughput, Comprehensive Single-Cell Proteomic Analysis of <i>Xenopus laevis</i> Embryos at the 50-Cell Stage Using a Microplate-Based MICROFASP System. <i>Analytical Chemistry</i> , 2022, 94, 3254-3259.	6.5	5
8	Rapid and Gentle Immunopurification of Brain Synaptic Vesicles. <i>Journal of Neuroscience</i> , 2022, 42, 3512-3522.	3.6	16
9	Severe COVID-19 Shares a Common Neutrophil Activation Signature with Other Acute Inflammatory States. <i>Cells</i> , 2022, 11, 847.	4.1	27
10	Comparative functional genomics identifies an iron-limited bottleneck in a <i>Saccharomyces cerevisiae</i> strain with a cytosolic-localized isobutanol pathway. <i>Synthetic and Systems Biotechnology</i> , 2022, 7, 738-749.	3.7	4
11	Practical Effects of Intramolecular Hydrogen Rearrangement in Electron Transfer Dissociation-Based Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 100-110.	2.8	2
12	High-fat diet disrupts REG3 β and gut microbial rhythms promoting metabolic dysfunction. <i>Cell Host and Microbe</i> , 2022, 30, 809-823.e6.	11.0	26
13	Three-dimensional structure determination of protein complexes using matrix-landing mass spectrometry. <i>Nature Communications</i> , 2022, 13, 2276.	12.8	31
14	Defining mitochondrial protein functions through deep multiomic profiling. <i>Nature</i> , 2022, 606, 382-388.	27.8	49
15	Large-Scale Multi-omic Analysis of COVID-19 Severity. <i>Cell Systems</i> , 2021, 12, 23-40.e7.	6.2	438
16	Defining intermediates and redundancies in coenzyme Q precursor biosynthesis. <i>Journal of Biological Chemistry</i> , 2021, 296, 100643.	3.4	12
17	Proteomics, Lipidomics, Metabolomics, and 16S DNA Sequencing of Dental Plaque From Patients With Diabetes and Periodontal Disease. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100126.	3.8	19
18	<i>Nras</i> <i>Q61R/+</i> and <i>Kras</i> Δ^{Δ} cooperate to downregulate Rasgrp1 and promote lympho-myeloid leukemia in early T-cell precursors. <i>Blood</i> , 2021, 137, 3259-3271.	1.4	5

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19	Multi-Omic Single-Shot Technology for Integrated Proteome and Lipidome Analysis. <i>Analytical Chemistry</i> , 2021, 93, 4217-4222.	6.5	22
20	Mapping of the contraction-induced phosphoproteome identifies TRIM28 as a significant regulator of skeletal muscle size and function. <i>Cell Reports</i> , 2021, 34, 108796.	6.4	36
21	Pilot proteomic analysis of cerebrospinal fluid in Alzheimer's disease. <i>Proteomics - Clinical Applications</i> , 2021, 15, e2000072.	1.6	5
22	A deep analysis of the proteomic and phosphoproteomic alterations that occur in skeletal muscle after the onset of immobilization. <i>Journal of Physiology</i> , 2021, 599, 2887-2906.	2.9	13
23	Metabolomic Biomarkers Differentiate Soy Sauce Freshness under Conditions of Accelerated Storage. <i>Journal of Food Quality</i> , 2021, 2021, 1-11.	2.6	1
24	The molecular and metabolic program by which white adipocytes adapt to cool physiologic temperatures. <i>PLoS Biology</i> , 2021, 19, e3000988.	5.6	11
25	Loss of C2orf69 defines a fatal autoinflammatory syndrome in humans and zebrafish that evokes a glycogen-storage-associated mitochondriopathy. <i>American Journal of Human Genetics</i> , 2021, 108, 1301-1317.	6.2	11
26	UbiB proteins regulate cellular CoQ distribution in <i>Saccharomyces cerevisiae</i> . <i>Nature Communications</i> , 2021, 12, 4769.	12.8	26
27	Carbomer-based adjuvant elicits CD8 T-cell immunity by inducing a distinct metabolic state in cross-presenting dendritic cells. <i>PLoS Pathogens</i> , 2021, 17, e1009168.	4.7	19
28	A network-based comparative framework to study conservation and divergence of proteomes in plant phylogenies. <i>Nucleic Acids Research</i> , 2021, 49, e3-e3.	14.5	5
29	Rapid preparation of human blood plasma for bottom-up proteomics analysis. <i>STAR Protocols</i> , 2021, 2, 100856.	1.2	2
30	Metabolic Remodeling during Nitrogen Fixation in <i>Zymomonas mobilis</i> . <i>MSystems</i> , 2021, 6, e0098721.	3.8	5
31	DNA-Scaffolded Synergistic Catalysis. <i>Journal of the American Chemical Society</i> , 2021, 143, 21402-21409.	13.7	12
32	Argonaut: A Web Platform for Collaborative Multi-omic Data Visualization and Exploration. <i>Patterns</i> , 2020, 1, 100122.	5.9	18
33	Quantitative shotgun proteome analysis by direct infusion. <i>Nature Methods</i> , 2020, 17, 1222-1228.	19.0	48
34	Global Phosphoproteome Analysis Using High-Field Asymmetric Waveform Ion Mobility Spectrometry on a Hybrid Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2020, 92, 15959-15967.	6.5	28
35	Optical Fiber-Enabled Photoactivation of Peptides and Proteins. <i>Analytical Chemistry</i> , 2020, 92, 12363-12370.	6.5	11
36	Discovering How Heme Controls Genome Function Through Heme-omics. <i>Cell Reports</i> , 2020, 31, 107832.	6.4	21

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37	Survival Following Traumatic Brain Injury in <i>Drosophila</i> Is Increased by Heterozygosity for a Mutation of the NF- κ B Innate Immune Response Transcription Factor Relish. <i>Genetics</i> , 2020, 216, 1117-1136.	2.9	16
38	Constructing and deconstructing GATA2-regulated cell fate programs to establish developmental trajectories. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	28
39	Phosphorylation controls RNA binding and transcription by the influenza virus polymerase. <i>PLoS Pathogens</i> , 2020, 16, e1008841.	4.7	17
40	A large-scale genome-wide lipid association map guides lipid identification. <i>Nature Metabolism</i> , 2020, 2, 1149-1162.	11.9	43
41	Production of hydrolysates from unmilled AFEX-pretreated switchgrass and comparative fermentation with <i>Zymomonas mobilis</i> . <i>Bioresource Technology Reports</i> , 2020, 11, 100517.	2.7	5
42	Mapping Physiological ADP-Ribosylation Using Activated Ion Electron Transfer Dissociation. <i>Cell Reports</i> , 2020, 32, 108176.	6.4	75
43	Post-Translation Regulation of Influenza Virus Replication. <i>Annual Review of Virology</i> , 2020, 7, 167-187.	6.7	12
44	Quantitative capillary zone electrophoresis-mass spectrometry reveals the <i>N</i> -glycome developmental plan during vertebrate embryogenesis. <i>Molecular Omics</i> , 2020, 16, 210-220.	2.8	5
45	Phosphoproteome Response to Dithiothreitol Reveals Unique <i>Versus</i> Shared Features of <i>Saccharomyces cerevisiae</i> Stress Responses. <i>Journal of Proteome Research</i> , 2020, 19, 3405-3417.	3.7	37
46	Top-Down Characterization of an Intact Monoclonal Antibody Using Activated Ion Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2020, 92, 10246-10251.	6.5	22
47	Ribonucleic Acid Sequence Characterization by Negative Electron Transfer Dissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 4436-4444.	6.5	19
48	Orosomucoid-like 3 Supports Rhinovirus Replication in Human Epithelial Cells. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2020, 62, 783-792.	2.9	20
49	Mass spectrometry proteomics reveals a function for mammalian CALCOCO1 in MTOR-regulated selective autophagy. <i>Autophagy</i> , 2020, 16, 2219-2237.	9.1	37
50	Assessing the Viability of Recovery of Hydroxycinnamic Acids from Lignocellulosic Biorefinery Alkaline Pretreatment Waste Streams. <i>ChemSusChem</i> , 2020, 13, 2012-2024.	6.8	54
51	A Genetic Toggle for Chemical Control of Individual Plk1 Substrates. <i>Cell Chemical Biology</i> , 2020, 27, 350-362.e8.	5.2	1
52	Broad and thematic remodeling of the surfaceome and glycoproteome on isogenic cells transformed with driving proliferative oncogenes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7764-7775.	7.1	54
53	Tailoring a Global Iron Regulon to a Uropathogen. <i>MBio</i> , 2020, 11, .	4.1	21
54	Assessing the Viability of Recovery of Hydroxycinnamic Acids from Lignocellulosic Biorefinery Alkaline Pretreatment Waste Streams. <i>ChemSusChem</i> , 2020, 13, 1922-1922.	6.8	0

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55	The genetic basis of aneuploidy tolerance in wild yeast. <i>ELife</i> , 2020, 9, .	6.0	61
56	Phosphorylation controls RNA binding and transcription by the influenza virus polymerase. , 2020, 16, e1008841.		0
57	Phosphorylation controls RNA binding and transcription by the influenza virus polymerase. , 2020, 16, e1008841.		0
58	Phosphorylation controls RNA binding and transcription by the influenza virus polymerase. , 2020, 16, e1008841.		0
59	Phosphorylation controls RNA binding and transcription by the influenza virus polymerase. , 2020, 16, e1008841.		0
60	Phosphorylation controls RNA binding and transcription by the influenza virus polymerase. , 2020, 16, e1008841.		0
61	Pptc7 is an essential phosphatase for promoting mammalian mitochondrial metabolism and biogenesis. <i>Nature Communications</i> , 2019, 10, 3197.	12.8	45
62	Accelerating Lipidomic Method Development through <i>in Silico</i> Simulation. <i>Analytical Chemistry</i> , 2019, 91, 9698-9706.	6.5	12
63	Genome Wide Phosphoproteome Analysis of <i>Zymomonas mobilis</i> Under Anaerobic, Aerobic, and N2-Fixing Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 1986.	3.5	13
64	Real-time health monitoring through urine metabolomics. <i>Npj Digital Medicine</i> , 2019, 2, 109.	10.9	39
65	Multiomic Fermentation Using Chemically Defined Synthetic Hydrolyzates Revealed Multiple Effects of Lignocellulose-Derived Inhibitors on Cell Physiology and Xylose Utilization in <i>Zymomonas mobilis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2596.	3.5	15
66	Acetyl-CoA flux regulates the proteome and acetyl-proteome to maintain intracellular metabolic crosstalk. <i>Nature Communications</i> , 2019, 10, 3929.	12.8	28
67	Genetic determinants of gut microbiota composition and bile acid profiles in mice. <i>PLoS Genetics</i> , 2019, 15, e1008073.	3.5	75
68	Maximizing Tandem Mass Spectrometry Acquisition Rates for Shotgun Proteomics. <i>Analytical Chemistry</i> , 2019, 91, 12625-12629.	6.5	10
69	Learning Drug Functions from Chemical Structures with Convolutional Neural Networks and Random Forests. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4438-4449.	5.4	61
70	Coenzyme Q biosynthetic proteins assemble in a substrate-dependent manner into domains at ERâ€“mitochondria contacts. <i>Journal of Cell Biology</i> , 2019, 218, 1353-1369.	5.2	69
71	S-adenosylmethionine biosynthesis is a targetable metabolic vulnerability of cancer stem cells. <i>Breast Cancer Research and Treatment</i> , 2019, 175, 39-50.	2.5	55
72	Single-Shot Capillary Zone Electrophoresisâ€“Tandem Mass Spectrometry Produces over 4400 Phosphopeptide Identifications from a 220 ng Sample. <i>Journal of Proteome Research</i> , 2019, 18, 3166-3173.	3.7	19

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73	Metabolic Remodeling during Biofilm Development of <i>Bacillus subtilis</i> . <i>MBio</i> , 2019, 10, .	4.1	93
74	PKA and HOG signaling contribute separable roles to anaerobic xylose fermentation in yeast engineered for biofuel production. <i>PLoS ONE</i> , 2019, 14, e0212389.	2.5	7
75	Interactive Peptide Spectral Annotator: A Versatile Web-based Tool for Proteomic Applications. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S193-S201.	3.8	97
76	Capillary Zone Electrophoresis-Tandem Mass Spectrometry with Activated Ion Electron Transfer Dissociation for Large-scale Top-down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2470-2479.	2.8	17
77	Capturing site-specific heterogeneity with large-scale N-glycoproteome analysis. <i>Nature Communications</i> , 2019, 10, 1311.	12.8	180
78	Rewired cellular signaling coordinates sugar and hypoxic responses for anaerobic xylose fermentation in yeast. <i>PLoS Genetics</i> , 2019, 15, e1008037.	3.5	26
79	Proteomic Atlas of the Human Brain in Alzheimer's Disease. <i>Journal of Proteome Research</i> , 2019, 18, 1380-1391.	3.7	42
80	Polo-like kinase 4 maintains centriolar satellite integrity by phosphorylation of centrosomal protein 131 (CEP131). <i>Journal of Biological Chemistry</i> , 2019, 294, 6531-6549.	3.4	18
81	Mapping Lipid Fragmentation for Tailored Mass Spectral Libraries. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 659-668.	2.8	16
82	Systems-Level Analysis of Oxygen Exposure in <i>Zymomonas mobilis</i> : Implications for Isoprenoid Production. <i>MSystems</i> , 2019, 4, .	3.8	27
83	Proteomic and transcriptomic analyses of early and late-chronic <i>Toxoplasma gondii</i> infection shows novel and stage specific transcripts. <i>BMC Genomics</i> , 2019, 20, 859.	2.8	35
84	OptSSeq explores enzyme expression and function landscapes to maximize isobutanol production rate. <i>Metabolic Engineering</i> , 2019, 52, 324-340.	7.0	36
85	An Isoprene Lipid-Binding Protein Promotes Eukaryotic Coenzyme Q Biosynthesis. <i>Molecular Cell</i> , 2019, 73, 763-774.e10.	9.7	37
86	MS-Helios: a Circos wrapper to visualize multi-omic datasets. <i>BMC Bioinformatics</i> , 2019, 20, 21.	2.6	9
87	Elucidating an Erythroblast Survival Mechanism: Differential Contributions of Exosome Complex Catalytic Subunits. <i>Blood</i> , 2019, 134, 155-155.	1.4	0
88	GATA2-Dependent Developmental and Regenerative Networks. <i>Blood</i> , 2019, 134, 1182-1182.	1.4	0
89	Caloric Restriction Engages Hepatic RNA Processing Mechanisms in Rhesus Monkeys. <i>Cell Metabolism</i> , 2018, 27, 677-688.e5.	16.2	56
90	Islet proteomics reveals genetic variation in dopamine production resulting in altered insulin secretion. <i>Journal of Biological Chemistry</i> , 2018, 293, 5860-5877.	3.4	43

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91	Expression of novel "LOCGEF" isoforms of ARHGEF18 in eosinophils. <i>Journal of Leukocyte Biology</i> , 2018, 104, 135-145.	3.3	3
92	Lignin Conversion to Low-Molecular-Weight Aromatics via an Aerobic Oxidation-Hydrolysis Sequence: Comparison of Different Lignin Sources. <i>ACS Sustainable Chemistry and Engineering</i> , 2018, 6, 3367-3374.	6.7	118
93	Identifying Novel Signaling Pathways: An Exercise Scientists Guide to Phosphoproteomics. <i>Exercise and Sport Sciences Reviews</i> , 2018, 46, 76-85.	3.0	5
94	Multi-omics Reveal Specific Targets of the RNA-Binding Protein Puf3p and Its Orchestration of Mitochondrial Biogenesis. <i>Cell Systems</i> , 2018, 6, 125-135.e6.	6.2	80
95	Improved Precursor Characterization for Data-Dependent Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 2333-2340.	6.5	65
96	Multiplexed proteome analysis with neutron-encoded stable isotope labeling in cells and mice. <i>Nature Protocols</i> , 2018, 13, 293-306.	12.0	35
97	An Autophagy-Independent Role for <i>ATG41</i> in Sulfur Metabolism During Zinc Deficiency. <i>Genetics</i> , 2018, 208, 1115-1130.	2.9	6
98	ATM directs DNA damage responses and proteostasis via genetically separable pathways. <i>Science Signaling</i> , 2018, 11, .	3.6	87
99	Proteomic and Phosphoproteomic Changes Induced by Prolonged Activation of Human Eosinophils with IL-3. <i>Journal of Proteome Research</i> , 2018, 17, 2102-2111.	3.7	11
100	Lipidex: An Integrated Software Package for High-Confidence Lipid Identification. <i>Cell Systems</i> , 2018, 6, 621-625.e5.	6.2	108
101	Sequencing Larger Intact Proteins (30-70 kDa) with Activated Ion Electron Transfer Dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 140-149.	2.8	51
102	The Role of Electron Transfer Dissociation in Modern Proteomics. <i>Analytical Chemistry</i> , 2018, 90, 40-64.	6.5	124
103	Conserved Lipid and Small-Molecule Modulation of COQ8 Reveals Regulation of the Ancient Kinase-like UbiB Family. <i>Cell Chemical Biology</i> , 2018, 25, 154-165.e11.	5.2	63
104	The cellular economy of the <i>Saccharomyces cerevisiae</i> zinc proteome. <i>Metallomics</i> , 2018, 10, 1755-1776.	2.4	66
105	The GIS2 Gene Is Repressed by a Zinc-Regulated Bicistronic RNA in <i>Saccharomyces cerevisiae</i> . <i>Genes</i> , 2018, 9, 462.	2.4	4
106	Production of Over 27 000 Peptide and Nearly 4400 Protein Identifications by Single-Shot Capillary-Zone Electrophoresis-Mass Spectrometry via Combination of a Very-Low-Electroosmosis Coated Capillary, a Third-Generation Electrokinetically-Pumped Sheath-Flow Nanospray Interface, an Orbitrap Fusion Lumos Tribrid Mass Spectrometer, and an Advanced-Peak-Determination Algorithm. <i>Analytical Chemistry</i> , 2018, 90, 12090-12093.	6.5	26
107	Ultra-High Pressure (>30,000 psi) Packing of Capillary Columns Enhancing Depth of Shotgun Proteomic Analyses. <i>Analytical Chemistry</i> , 2018, 90, 11503-11508.	6.5	62
108	Network inference reveals novel connections in pathways regulating growth and defense in the yeast salt response. <i>PLoS Computational Biology</i> , 2018, 13, e1006088.	3.2	23

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109	Comprehensive Single-Shot Proteomics with FAIMS on a Hybrid Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2018, 90, 9529-9537.	6.5	218
110	Top-Down Characterization of Proteins with Intact Disulfide Bonds Using Activated-Ion Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2018, 90, 8946-8953.	6.5	22
111	The Value of Activated Ion Electron Transfer Dissociation for High-Throughput Top-Down Characterization of Intact Proteins. <i>Analytical Chemistry</i> , 2018, 90, 8553-8560.	6.5	35
112	Decoupling Yeast Cell Division and Stress Defense Implicates mRNA Repression in Translational Reallocation during Stress. <i>Current Biology</i> , 2018, 28, 2673-2680.e4.	3.9	42
113	Chemical genomic guided engineering of gamma-valerolactone tolerant yeast. <i>Microbial Cell Factories</i> , 2018, 17, 5.	4.0	14
114	Complete genome sequence and the expression pattern of plasmids of the model ethanologen <i>Zymomonas mobilis</i> ZM4 and its xylose-utilizing derivatives 8b and 2032. <i>Biotechnology for Biofuels</i> , 2018, 11, 125.	6.2	79
115	Diverse lignocellulosic feedstocks can achieve high field-scale ethanol yields while providing flexibility for the biorefinery and landscape-level environmental benefits. <i>GCB Bioenergy</i> , 2018, 10, 825-840.	5.6	31
116	GATA/Heme Multi-omics Reveals a Trace Metal-Dependent Cellular Differentiation Mechanism. <i>Developmental Cell</i> , 2018, 46, 581-594.e4.	7.0	31
117	Genetic Regulation of Plasma Lipid Species and Their Association with Metabolic Phenotypes. <i>Cell Systems</i> , 2018, 6, 709-721.e6.	6.2	52
118	Systems Analyses Reveal Physiological Roles and Genetic Regulators of Liver Lipid Species. <i>Cell Systems</i> , 2018, 6, 722-733.e6.	6.2	54
119	GATA/Heme Multi-Omics Reveals a Trace Metal-Dependent Erythrocyte Developmental Mechanism. <i>Blood</i> , 2018, 132, 500-500.	1.4	0
120	Ptc7p Dephosphorylates Select Mitochondrial Proteins to Enhance Metabolic Function. <i>Cell Reports</i> , 2017, 18, 307-313.	6.4	45
121	Identification of the phosphorylation targets of symbiotic receptor-like kinases using a high-throughput multiplexed assay for kinase specificity. <i>Plant Journal</i> , 2017, 90, 1196-1207.	5.7	15
122	Activated Ion-Electron Transfer Dissociation Enables Comprehensive Top-Down Protein Fragmentation. <i>Journal of Proteome Research</i> , 2017, 16, 2653-2659.	3.7	60
123	Negative Electron Transfer Dissociation Sequencing of Increasingly Sulfated Glycosaminoglycan Oligosaccharides on an Orbitrap Mass Spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 1844-1854.	2.8	44
124	A map of the phosphoproteomic alterations that occur after a bout of maximal-intensity contractions. <i>Journal of Physiology</i> , 2017, 595, 5209-5226.	2.9	70
125	Global mapping of CARM1 substrates defines enzyme specificity and substrate recognition. <i>Nature Communications</i> , 2017, 8, 15571.	12.8	100
126	Integrative proteomics and biochemical analyses define Ptc6p as the <i>Saccharomyces cerevisiae</i> pyruvate dehydrogenase phosphatase. <i>Journal of Biological Chemistry</i> , 2017, 292, 11751-11759.	3.4	25

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127	Sulfur Pentafluoride is a Preferred Reagent Cation for Negative Electron Transfer Dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 1324-1332.	2.8	8
128	Phosphoproteomics with Activated Ion Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2017, 89, 6367-6376.	6.5	44
129	Implementation of Activated Ion Electron Transfer Dissociation on a Quadrupole-Orbitrap-Linear Ion Trap Hybrid Mass Spectrometer. <i>Analytical Chemistry</i> , 2017, 89, 6358-6366.	6.5	41
130	The dental calculus metabolome in modern and historic samples. <i>Metabolomics</i> , 2017, 13, 134.	3.0	44
131	A Split-Abl Kinase for Direct Activation in Cells. <i>Cell Chemical Biology</i> , 2017, 24, 1250-1258.e4.	5.2	12
132	GATA Factor-Regulated Samd14 Enhancer Confers Red Blood Cell Regeneration and Survival in Severe Anemia. <i>Developmental Cell</i> , 2017, 42, 213-225.e4.	7.0	29
133	Gender Diversity in a STEM Subfield â€“ Analysis of a Large Scientific Society and Its Annual Conferences. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 2523-2531.	2.8	27
134	Multi-omic Mitoprotease Profiling Defines a Role for Oct1p in Coenzyme Q Production. <i>Molecular Cell</i> , 2017, 68, 970-977.e11.	9.7	45
135	Phosphorylation Dynamics Dominate the Regulated Proteome during Early <i>Xenopus</i> Development. <i>Scientific Reports</i> , 2017, 7, 15647.	3.3	24
136	Proteomics of Eosinophil Activation. <i>Frontiers in Medicine</i> , 2017, 4, 159.	2.6	6
137	Erythropoietin signaling regulates heme biosynthesis. <i>ELife</i> , 2017, 6, .	6.0	36
138	Influenza virus recruits host protein kinase C to control assembly and activity of its replication machinery. <i>ELife</i> , 2017, 6, .	6.0	57
139	Genome Sequence and Analysis of a Stress-Tolerant, Wild-Derived Strain of <i>Saccharomyces cerevisiae</i> Used in Biofuels Research. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1757-1766.	1.8	61
140	Inhibition of microbial biofuel production in drought-stressed switchgrass hydrolysate. <i>Biotechnology for Biofuels</i> , 2016, 9, 237.	6.2	46
141	Proteomics Moves into the Fast Lane. <i>Cell Systems</i> , 2016, 2, 142-143.	6.2	37
142	Decoding Polo-like kinase 1 signaling along the kinetochoreâ€“centromere axis. <i>Nature Chemical Biology</i> , 2016, 12, 411-418.	8.0	40
143	The Peripheral Blood Eosinophil Proteome. <i>Journal of Proteome Research</i> , 2016, 15, 1524-1533.	3.7	79
144	Mechanism of imidazolium ionic liquids toxicity in <i>Saccharomyces cerevisiae</i> and rational engineering of a tolerant, xylose-fermenting strain. <i>Microbial Cell Factories</i> , 2016, 15, 17.	4.0	67

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145	Mitochondrial protein functions elucidated by multi-omic mass spectrometry profiling. <i>Nature Biotechnology</i> , 2016, 34, 1191-1197.	17.5	122
146	Mitochondrial Protein Interaction Mapping Identifies Regulators of Respiratory Chain Function. <i>Molecular Cell</i> , 2016, 63, 621-632.	9.7	241
147	Valosin-containing protein (VCP)â€“Adaptor Interactions are Exceptionally Dynamic and Subject to Differential Modulation by a VCP Inhibitor. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2970-2986.	3.8	42
148	Cerebellar Ataxia and Coenzyme Q Deficiency through Loss of Unorthodox Kinase Activity. <i>Molecular Cell</i> , 2016, 63, 608-620.	9.7	101
149	NeuCode Proteomics Reveals Bap1 Regulation of Metabolism. <i>Cell Reports</i> , 2016, 16, 583-595.	6.4	57
150	Full-Featured Search Algorithm for Negative Electron-Transfer Dissociation. <i>Journal of Proteome Research</i> , 2016, 15, 2768-2776.	3.7	9
151	A proteomic atlas of the legume <i>Medicago truncatula</i> and its nitrogen-fixing endosymbiont <i>Sinorhizobium meliloti</i> . <i>Nature Biotechnology</i> , 2016, 34, 1198-1205.	17.5	133
152	Now, More Than Ever, Proteomics Needs Better Chromatography. <i>Cell Systems</i> , 2016, 3, 321-324.	6.2	117
153	Multi-omics Evidence for Inheritance of Energy Pathways in Red Blood Cells. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3614-3623.	3.8	18
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