Joshua J Coon

List of Publications by Year
in descending order

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284 papers	23,069 citations	12597 71 h-index	12272 138 g-index
306 all docs	306 docs citations	306 times ranked	28284 citing authors

#	Article	IF	Citations
1	Proteomic and metabolomic profiling of acute and chronic stress events associated with military exercises. Molecular Omics, 2022, 18, 279-295.	1.4	4
2	Multi-omics analysis identifies essential regulators of mitochondrial stress response in two wild-type C.Âelegans strains. IScience, 2022, 25, 103734.	1.9	9
3	Tcof1 haploinsufficiency promotes early T cell precursor-like leukemia in NrasQ61R/+ mice. Leukemia, 2022, , .	3.3	0
4	Rapid Targeted Quantitation of Protein Overexpression with Direct Infusion Shotgun Proteome Analysis (DISPA-PRM). Analytical Chemistry, 2022, 94, 1965-1973.	3.2	8
5	Maximizing MS/MS Acquisition for Lipidomics Using Capillary Separation and Orbitrap Tribrid Mass Spectrometer. Analytical Chemistry, 2022, 94, 3394-3399.	3.2	9
6	Infrared Photoactivation Boosts Reporter Ion Yield in Isobaric Tagging. Analytical Chemistry, 2022, , .	3.2	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. Analytical Chemistry, 2022, 94, 3254-3259.	3.2	5
8	Rapid and Gentle Immunopurification of Brain Synaptic Vesicles. Journal of Neuroscience, 2022, 42, 3512-3522.	1.7	16
9	Severe COVID-19 Shares a Common Neutrophil Activation Signature with Other Acute Inflammatory States. Cells, 2022, 11, 847.	1.8	27
10	Comparative functional genomics identifies an iron-limited bottleneck in a Saccharomyces cerevisiae strain with a cytosolic-localized isobutanol pathway. Synthetic and Systems Biotechnology, 2022, 7, 738-749.	1.8	4
11	Practical Effects of Intramolecular Hydrogen Rearrangement in Electron Transfer Dissociation-Based Proteomics. Journal of the American Society for Mass Spectrometry, 2022, 33, 100-110.	1.2	2
12	High-fat diet disrupts REG3Î³ and gut microbial rhythms promoting metabolic dysfunction. Cell Host and Microbe, 2022, 30, 809-823.e6.	5.1	26
13	Three-dimensional structure determination of protein complexes using matrix-landing mass spectrometry. Nature Communications, 2022, 13, 2276.	5.8	31
14	Defining mitochondrial protein functions through deep multiomic profiling. Nature, 2022, 606, 382-388.	13.7	49
15	Large-Scale Multi-omic Analysis of COVID-19 Severity. Cell Systems, 2021, 12, 23-40.e7.	2.9	438
16	Defining intermediates and redundancies in coenzyme Q precursor biosynthesis. Journal of Biological Chemistry, 2021, 296, 100643.	1.6	12
17	Proteomics, Lipidomics, Metabolomics, and 16S DNA Sequencing of Dental Plaque From Patients With Diabetes and Periodontal Disease. Molecular and Cellular Proteomics, 2021, 20, 100126.	2.5	19
18	<i>Nras</i> <i>Q61R/+</i> and <i>Kras</i> <i>â^’/â^’</i> cooperate to downregulate Rasgrp1 and promote lympho-myeloid leukemia in early T-cell precursors. Blood, 2021, 137, 3259-3271.	0.6	5

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19	Multi-Omic Single-Shot Technology for Integrated Proteome and Lipidome Analysis. Analytical Chemistry, 2021, 93, 4217-4222.	3.2	22
20	Mapping of the contraction-induced phosphoproteome identifies TRIM28 as a significant regulator of skeletal muscle size and function. Cell Reports, 2021, 34, 108796.	2.9	36
21	Pilot proteomic analysis of cerebrospinal fluid in Alzheimer's disease. Proteomics - Clinical Applications, 2021, 15, e2000072.	0.8	5
22	A deep analysis of the proteomic and phosphoproteomic alterations that occur in skeletal muscle after the onset of immobilization. Journal of Physiology, 2021, 599, 2887-2906.	1.3	13
23	Metabolomic Biomarkers Differentiate Soy Sauce Freshness under Conditions of Accelerated Storage. Journal of Food Quality, 2021, 2021, 1-11.	1.4	1
24	The molecular and metabolic program by which white adipocytes adapt to cool physiologic temperatures. PLoS Biology, 2021, 19, e3000988.	2.6	11
25	Loss of C2orf69 defines a fatal autoinflammatory syndrome in humans and zebrafish that evokes a glycogen-storage-associated mitochondriopathy. American Journal of Human Genetics, 2021, 108, 1301-1317.	2.6	11
26	UbiB proteins regulate cellular CoQ distribution in Saccharomyces cerevisiae. Nature Communications, 2021, 12, 4769.	5.8	26
27	Carbomer-based adjuvant elicits CD8 T-cell immunity by inducing a distinct metabolic state in cross-presenting dendritic cells. PLoS Pathogens, 2021, 17, e1009168.	2.1	19
28	A network-based comparative framework to study conservation and divergence of proteomes in plant phylogenies. Nucleic Acids Research, 2021, 49, e3-e3.	6.5	5
29	Rapid preparation of human blood plasma for bottom-up proteomics analysis. STAR Protocols, 2021, 2, 100856.	0.5	2
30	Metabolic Remodeling during Nitrogen Fixation in Zymomonas mobilis. MSystems, 2021, 6, e0098721.	1.7	5
31	DNA-Scaffolded Synergistic Catalysis. Journal of the American Chemical Society, 2021, 143, 21402-21409.	6.6	12
32	Argonaut: A Web Platform for Collaborative Multi-omic Data Visualization and Exploration. Patterns, 2020, 1, 100122.	3.1	18
33	Quantitative shotgun proteome analysis by direct infusion. Nature Methods, 2020, 17, 1222-1228.	9.0	48
34	Global Phosphoproteome Analysis Using High-Field Asymmetric Waveform Ion Mobility Spectrometry on a Hybrid Orbitrap Mass Spectrometer. Analytical Chemistry, 2020, 92, 15959-15967.	3.2	28
35	Optical Fiber-Enabled Photoactivation of Peptides and Proteins. Analytical Chemistry, 2020, 92, 12363-12370.	3.2	11
36	Discovering How Heme Controls Genome Function Through Heme-omics. Cell Reports, 2020, 31, 107832.	2.9	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-ÎºB Innate Immune Response Transcription Factor Relish. Genetics, 2020, 216, 1117-1136.	1.2	16
38	Constructing and deconstructing GATA2-regulated cell fate programs to establish developmental trajectories. Journal of Experimental Medicine, 2020, 217, .	4.2	28
39	Phosphorylation controls RNA binding and transcription by the influenza virus polymerase. PLoS Pathogens, 2020, 16, e1008841.	2.1	17
40	A large-scale genomeâ€"lipid association map guides lipid identification. Nature Metabolism, 2020, 2, 1149-1162.	5.1	43
41	Production of hydrolysates from unmilled AFEX-pretreated switchgrass and comparative fermentation with Zymomonas mobilis. Bioresource Technology Reports, 2020, 11, 100517.	1.5	5
42	Mapping Physiological ADP-Ribosylation Using Activated Ion Electron Transfer Dissociation. Cell Reports, 2020, 32, 108176.	2.9	75
43	Post-Translation Regulation of Influenza Virus Replication. Annual Review of Virology, 2020, 7, 167-187.	3.0	12
44	Quantitative capillary zone electrophoresis-mass spectrometry reveals the <i>N</i>-glycome developmental plan during vertebrate embryogenesis. Molecular Omics, 2020, 16, 210-220.	1.4	5
45	Phosphoproteome Response to Dithiothreitol Reveals Unique <i>Versus</i> Shared Features of <i>Saccharomyces cerevisiae</i> Stress Responses. Journal of Proteome Research, 2020, 19, 3405-3417.	1.8	37
46	Top-Down Characterization of an Intact Monoclonal Antibody Using Activated Ion Electron Transfer Dissociation. Analytical Chemistry, 2020, 92, 10246-10251.	3.2	22
47	Ribonucleic Acid Sequence Characterization by Negative Electron Transfer Dissociation Mass Spectrometry. Analytical Chemistry, 2020, 92, 4436-4444.	3.2	19
48	Orosomucoid-like 3 Supports Rhinovirus Replication in Human Epithelial Cells. American Journal of Respiratory Cell and Molecular Biology, 2020, 62, 783-792.	1.4	20
49	Mass spectrometry proteomics reveals a function for mammalian CALCOCO1 in MTOR-regulated selective autophagy. Autophagy, 2020, 16, 2219-2237.	4.3	37
50	Assessing the Viability of Recovery of Hydroxycinnamic Acids from Lignocellulosic Biorefinery Alkaline Pretreatment Waste Streams. ChemSusChem, 2020, 13, 2012-2024.	3.6	54
51	A Genetic Toggle for Chemical Control of Individual Plk1 Substrates. Cell Chemical Biology, 2020, 27, 350-362.e8.	2.5	1
52	Broad and thematic remodeling of the surfaceome and glycoproteome on isogenic cells transformed with driving proliferative oncogenes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7764-7775.	3.3	54
53	Tailoring a Global Iron Regulon to a Uropathogen. MBio, 2020, 11, .	1.8	21
54	Assessing the Viability of Recovery of Hydroxycinnamic Acids from Lignocellulosic Biorefinery Alkaline Pretreatment Waste Streams. ChemSusChem, 2020, 13, 1922-1922.	3.6	0

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55	The genetic basis of aneuploidy tolerance in wild yeast. ELife, 2020, 9, .	2.8	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. Nature Communications, 2019, 10, 3197.	5.8	45
62	Accelerating Lipidomic Method Development through <i>in Silico</i> Simulation. Analytical Chemistry, 2019, 91, 9698-9706.	3.2	12
63	Genome Wide Phosphoproteome Analysis of Zymomonas mobilis Under Anaerobic, Aerobic, and N2-Fixing Conditions. Frontiers in Microbiology, 2019, 10, 1986.	1.5	13
64	Real-time health monitoring through urine metabolomics. Npj Digital Medicine, 2019, 2, 109.	5.7	39
65	Multiomic Fermentation Using Chemically Defined Synthetic Hydrolyzates Revealed Multiple Effects of Lignocellulose-Derived Inhibitors on Cell Physiology and Xylose Utilization in Zymomonas mobilis. Frontiers in Microbiology, 2019, 10, 2596.	1.5	15
66	Acetyl-CoA flux regulates the proteome and acetyl-proteome to maintain intracellular metabolic crosstalk. Nature Communications, 2019, 10, 3929.	5.8	28
67	Genetic determinants of gut microbiota composition and bile acid profiles in mice. PLoS Genetics, 2019, 15, e1008073.	1.5	75
68	Maximizing Tandem Mass Spectrometry Acquisition Rates for Shotgun Proteomics. Analytical Chemistry, 2019, 91, 12625-12629.	3.2	10
69	Learning Drug Functions from Chemical Structures with Convolutional Neural Networks and Random Forests. Journal of Chemical Information and Modeling, 2019, 59, 4438-4449.	2.5	61
70	Coenzyme Q biosynthetic proteins assemble in a substrate-dependent manner into domains at ERâ€“mitochondria contacts. Journal of Cell Biology, 2019, 218, 1353-1369.	2.3	69
71	S-adenosylmethionine biosynthesis is a targetable metabolic vulnerability of cancer stem cells. Breast Cancer Research and Treatment, 2019, 175, 39-50.	1.1	55
72	Single-Shot Capillary Zone Electrophoresisâ€“Tandem Mass Spectrometry Produces over 4400 Phosphopeptide Identifications from a 220 ng Sample. Journal of Proteome Research, 2019, 18, 3166-3173.	1.8	19

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73	Metabolic Remodeling during Biofilm Development of Bacillus subtilis. MBio, 2019, 10, .	1.8	93
74	PKA and HOG signaling contribute separable roles to anaerobic xylose fermentation in yeast engineered for biofuel production. PLoS ONE, 2019, 14, e0212389.	1.1	7
75	Interactive Peptide Spectral Annotator: A Versatile Web-based Tool for Proteomic Applications. Molecular and Cellular Proteomics, 2019, 18, S193-S201.	2.5	97
76	Capillary Zone Electrophoresis-Tandem Mass Spectrometry with Activated Ion Electron Transfer Dissociation for Large-scale Top-down Proteomics. Journal of the American Society for Mass Spectrometry, 2019, 30, 2470-2479.	1.2	17
77	Capturing site-specific heterogeneity with large-scale N-glycoproteome analysis. Nature Communications, 2019, 10, 1311.	5.8	180
78	Rewired cellular signaling coordinates sugar and hypoxic responses for anaerobic xylose fermentation in yeast. PLoS Genetics, 2019, 15, e1008037.	1.5	26
79	Proteomic Atlas of the Human Brain in Alzheimerâ€™s Disease. Journal of Proteome Research, 2019, 18, 1380-1391.	1.8	42
80	Polo-like kinase 4 maintains centriolar satellite integrity by phosphorylation of centrosomal protein 131 (CEP131). Journal of Biological Chemistry, 2019, 294, 6531-6549.	1.6	18
81	Mapping Lipid Fragmentation for Tailored Mass Spectral Libraries. Journal of the American Society for Mass Spectrometry, 2019, 30, 659-668.	1.2	16
82	Systems-Level Analysis of Oxygen Exposure in <i>Zymomonas mobilis</i> : Implications for Isoprenoid Production. MSystems, 2019, 4, .	1.7	27
83	Proteomic and transcriptomic analyses of early and late-chronic Toxoplasma gondii infection shows novel and stage specific transcripts. BMC Genomics, 2019, 20, 859.	1.2	35
84	OptSSeq explores enzyme expression and function landscapes to maximize isobutanol production rate. Metabolic Engineering, 2019, 52, 324-340.	3.6	36
85	An Isoprene Lipid-Binding Protein Promotes Eukaryotic Coenzyme Q Biosynthesis. Molecular Cell, 2019, 73, 763-774.e10.	4.5	37
86	MS-Helios: a Circos wrapper to visualize multi-omic datasets. BMC Bioinformatics, 2019, 20, 21.	1.2	9
87	Elucidating an Erythroblast Survival Mechanism: Differential Contributions of Exosome Complex Catalytic Subunits. Blood, 2019, 134, 155-155.	0.6	0
88	GATA2-Dependent Developmental and Regenerative Networks. Blood, 2019, 134, 1182-1182.	0.6	0
89	Caloric Restriction Engages Hepatic RNA Processing Mechanisms in Rhesus Monkeys. Cell Metabolism, 2018, 27, 677-688.e5.	7.2	56
90	Islet proteomics reveals genetic variation in dopamine production resulting in altered insulin secretion. Journal of Biological Chemistry, 2018, 293, 5860-5877.	1.6	43

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91	Expression of novel â€œLOCGEFâ€•isoforms of ARHGEF18 in eosinophils. Journal of Leukocyte Biology, 2018, 104, 135-145.	1.5	3
92	Lignin Conversion to Low-Molecular-Weight Aromatics via an Aerobic Oxidation-Hydrolysis Sequence: Comparison of Different Lignin Sources. ACS Sustainable Chemistry and Engineering, 2018, 6, 3367-3374.	3.2	118
93	Identifying Novel Signaling Pathways: An Exercise Scientists Guide to Phosphoproteomics. Exercise and Sport Sciences Reviews, 2018, 46, 76-85.	1.6	5
94	Multi-omics Reveal Specific Targets of the RNA-Binding Protein Puf3p and Its Orchestration of Mitochondrial Biogenesis. Cell Systems, 2018, 6, 125-135.e6.	2.9	80
95	Improved Precursor Characterization for Data-Dependent Mass Spectrometry. Analytical Chemistry, 2018, 90, 2333-2340.	3.2	65
96	Multiplexed proteome analysis with neutron-encoded stable isotope labeling in cells and mice. Nature Protocols, 2018, 13, 293-306.	5.5	35
97	An Autophagy-Independent Role for <i>ATG41</i> in Sulfur Metabolism During Zinc Deficiency. Genetics, 2018, 208, 1115-1130.	1.2	6
98	ATM directs DNA damage responses and proteostasis via genetically separable pathways. Science Signaling, 2018, 11, .	1.6	87
99	Proteomic and Phosphoproteomic Changes Induced by Prolonged Activation of Human Eosinophils with IL-3. Journal of Proteome Research, 2018, 17, 2102-2111.	1.8	11
100	LipiDex: An Integrated Software Package for High-Confidence Lipid Identification. Cell Systems, 2018, 6, 621-625.e5.	2.9	108
101	Sequencing Larger Intact Proteins (30-70 kDa) with Activated Ion Electron Transfer Dissociation. Journal of the American Society for Mass Spectrometry, 2018, 29, 140-149.	1.2	51
102	The Role of Electron Transfer Dissociation in Modern Proteomics. Analytical Chemistry, 2018, 90, 40-64.	3.2	124
103	Conserved Lipid and Small-Molecule Modulation of COQ8 Reveals Regulation of the Ancient Kinase-like UbiB Family. Cell Chemical Biology, 2018, 25, 154-165.e11.	2.5	63
104	The cellular economy of the <i>Saccharomyces cerevisiae</i> zinc proteome. Metallomics, 2018, 10, 1755-1776.	1.0	66
105	The GIS2 Gene Is Repressed by a Zinc-Regulated Bicistronic RNA in Saccharomyces cerevisiae. Genes, 2018, 9, 462.	1.0	4
106	Production of Over 27 000 Peptide and Nearly 4400 Protein Identifications by Single-Shot Capillary-Zone Electrophoresisâ€"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. Analytical Chemistry, 2018, 90, 12090-12093.	3.2	26
107	Ultra-High Pressure (>30,000 psi) Packing of Capillary Columns Enhancing Depth of Shotgun Proteomic Analyses. Analytical Chemistry, 2018, 90, 11503-11508.	3.2	62
108	Network inference reveals novel connections in pathways regulating growth and defense in the yeast salt response. PLoS Computational Biology, 2018, 13, e1006088.	1.5	23

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109	Comprehensive Single-Shot Proteomics with FAIMS on a Hybrid Orbitrap Mass Spectrometer. Analytical Chemistry, 2018, 90, 9529-9537.	3.2	218
110	Top-Down Characterization of Proteins with Intact Disulfide Bonds Using Activated-Ion Electron Transfer Dissociation. Analytical Chemistry, 2018, 90, 8946-8953.	3.2	22
111	The Value of Activated Ion Electron Transfer Dissociation for High-Throughput Top-Down Characterization of Intact Proteins. Analytical Chemistry, 2018, 90, 8553-8560.	3.2	35
112	Decoupling Yeast Cell Division and Stress Defense Implicates mRNA Repression in Translational Reallocation during Stress. Current Biology, 2018, 28, 2673-2680.e4.	1.8	42
113	Chemical genomic guided engineering of gamma-valerolactone tolerant yeast. Microbial Cell Factories, 2018, 17, 5.	1.9	14
114	Complete genome sequence and the expression pattern of plasmids of the model ethanologen Zymomonas mobilis ZM4 and its xylose-utilizing derivatives 8b and 2032. Biotechnology for Biofuels, 2018, 11, 125.	6.2	79
115	Diverse lignocellulosic feedstocks can achieve high fieldâ€scale ethanol yields while providing flexibility for the biorefinery and landscapeâ€level environmental benefits. GCB Bioenergy, 2018, 10, 825-840.	2.5	31
116	GATA/Heme Multi-omics Reveals a Trace Metal-Dependent Cellular Differentiation Mechanism. Developmental Cell, 2018, 46, 581-594.e4.	3.1	31
117	Genetic Regulation of Plasma Lipid Species and Their Association with Metabolic Phenotypes. Cell Systems, 2018, 6, 709-721.e6.	2.9	52
118	Systems Analyses Reveal Physiological Roles and Genetic Regulators of Liver Lipid Species. Cell Systems, 2018, 6, 722-733.e6.	2.9	54
119	GATA/Heme Multi-Omics Reveals a Trace Metal-Dependent Erythrocyte Developmental Mechanism. Blood, 2018, 132, 500-500.	0.6	0
120	Ptc7p Dephosphorylates Select Mitochondrial Proteins to Enhance Metabolic Function. Cell Reports, 2017, 18, 307-313.	2.9	45
121	Identification of the phosphorylation targets of symbiotic receptorâ€like kinases using a highâ€throughput multiplexed assay for kinase specificity. Plant Journal, 2017, 90, 1196-1207.	2.8	15
122	Activated Ion-Electron Transfer Dissociation Enables Comprehensive Top-Down Protein Fragmentation. Journal of Proteome Research, 2017, 16, 2653-2659.	1.8	60
123	Negative Electron Transfer Dissociation Sequencing of Increasingly Sulfated Glycosaminoglycan Oligosaccharides on an Orbitrap Mass Spectrometer. Journal of the American Society for Mass Spectrometry, 2017, 28, 1844-1854.	1.2	44
124	A map of the phosphoproteomic alterations that occur after a bout of maximalâ€intensity contractions. Journal of Physiology, 2017, 595, 5209-5226.	1.3	70
125	Global mapping of CARM1 substrates defines enzyme specificity and substrate recognition. Nature Communications, 2017, 8, 15571.	5.8	100
126	Integrative proteomics and biochemical analyses define Ptc6p as the Saccharomyces cerevisiae pyruvate dehydrogenase phosphatase. Journal of Biological Chemistry, 2017, 292, 11751-11759.	1.6	25

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127	Sulfur Pentafluoride is a Preferred Reagent Cation for Negative Electron Transfer Dissociation. Journal of the American Society for Mass Spectrometry, 2017, 28, 1324-1332.	1.2	8
128	Phosphoproteomics with Activated Ion Electron Transfer Dissociation. Analytical Chemistry, 2017, 89, 6367-6376.	3.2	44
129	Implementation of Activated Ion Electron Transfer Dissociation on a Quadrupole-Orbitrap-Linear Ion Trap Hybrid Mass Spectrometer. Analytical Chemistry, 2017, 89, 6358-6366.	3.2	41
130	The dental calculus metabolome in modern and historic samples. Metabolomics, 2017, 13, 134.	1.4	44
131	A Split-Abl Kinase for Direct Activation in Cells. Cell Chemical Biology, 2017, 24, 1250-1258.e4.	2.5	12
132	GATA Factor-Regulated Samd14 Enhancer Confers Red Blood Cell Regeneration and Survival in Severe Anemia. Developmental Cell, 2017, 42, 213-225.e4.	3.1	29
133	Gender Diversity in a STEM Subfield â€“ Analysis of a Large Scientific Society and Its Annual Conferences. Journal of the American Society for Mass Spectrometry, 2017, 28, 2523-2531.	1.2	27
134	Multi-omic Mitoprotease Profiling Defines a Role for Oct1p in Coenzyme Q Production. Molecular Cell, 2017, 68, 970-977.e11.	4.5	45
135	Phosphorylation Dynamics Dominate the Regulated Proteome during Early Xenopus Development. Scientific Reports, 2017, 7, 15647.	1.6	24
136	Proteomics of Eosinophil Activation. Frontiers in Medicine, 2017, 4, 159.	1.2	6
137	Erythropoietin signaling regulates heme biosynthesis. ELife, 2017, 6, .	2.8	36
138	Influenza virus recruits host protein kinase C to control assembly and activity of its replication machinery. ELife, 2017, 6, .	2.8	57
139	Genome Sequence and Analysis of a Stress-Tolerant, Wild-Derived Strain of Saccharomyces cerevisiae Used in Biofuels Research. G3: Genes, Genomes, Genetics, 2016, 6, 1757-1766.	0.8	61
140	Inhibition of microbial biofuel production in drought-stressed switchgrass hydrolysate. Biotechnology for Biofuels, 2016, 9, 237.	6.2	46
141	Proteomics Moves into the Fast Lane. Cell Systems, 2016, 2, 142-143.	2.9	37
142	Decoding Polo-like kinase 1 signaling along the kinetochoreâ€“centromere axis. Nature Chemical Biology, 2016, 12, 411-418.	3.9	40
143	The Peripheral Blood Eosinophil Proteome. Journal of Proteome Research, 2016, 15, 1524-1533.	1.8	79
144	Mechanism of imidazolium ionic liquids toxicity in Saccharomyces cerevisiae and rational engineering of a tolerant, xylose-fermenting strain. Microbial Cell Factories, 2016, 15, 17.	1.9	67

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145	Mitochondrial protein functions elucidated by multi-omic mass spectrometry profiling. Nature Biotechnology, 2016, 34, 1191-1197.	9.4	122
146	Mitochondrial Protein Interaction Mapping Identifies Regulators of Respiratory Chain Function. Molecular Cell, 2016, 63, 621-632.	4.5	241
147	Valosin-containing protein (VCP)â€"Adaptor Interactions are Exceptionally Dynamic and Subject to Differential Modulation by a VCP Inhibitor. Molecular and Cellular Proteomics, 2016, 15, 2970-2986.	2.5	42
148	Cerebellar Ataxia and Coenzyme Q Deficiency through Loss of Unorthodox Kinase Activity. Molecular Cell, 2016, 63, 608-620.	4.5	101
149	NeuCode Proteomics Reveals Bap1 Regulation of Metabolism. Cell Reports, 2016, 16, 583-595.	2.9	57
150	Full-Featured Search Algorithm for Negative Electron-Transfer Dissociation. Journal of Proteome Research, 2016, 15, 2768-2776.	1.8	9
151	A proteomic atlas of the legume Medicago truncatula and its nitrogen-fixing endosymbiont Sinorhizobium meliloti. Nature Biotechnology, 2016, 34, 1198-1205.	9.4	133
152	Now, More Than Ever, Proteomics Needs Better Chromatography. Cell Systems, 2016, 3, 321-324.	2.9	117
153	Multi-omics Evidence for Inheritance of Energy Pathways in Red Blood Cells. Molecular and Cellular Proteomics, 2016, 15, 3614-3623.	2.5	18
154	Quantifying pretreatment degradation compounds in solution and accumulated by cells during solids and yeast recycling in the Rapid Bioconversion with Integrated recycling Technology process using AFEXâ„¢ corn stover. Bioresource Technology, 2016, 205, 24-33.	4.8	17
155	Neucode Labels for Multiplexed, Absolute Protein Quantification. Analytical Chemistry, 2016, 88, 3295-3303.	3.2	23
156	Enhanced Dissociation of Intact Proteins with High Capacity Electron Transfer Dissociation. Journal of the American Society for Mass Spectrometry, 2016, 27, 520-531.	1.2	51
157	Phosphoproteomics in the Age of Rapid and Deep Proteome Profiling. Analytical Chemistry, 2016, 88, 74-94.	3.2	217
158	Mitochondrial protein hyperacetylation in the failing heart. JCI Insight, 2016, 1, .	2.3	133
159	Multi-Omics Evidence for Inheritance of Energy Pathways in Red Blood Cells. Blood, 2016, 128, 3838-3838.	0.6	0
160	Protein Composition of Infectious Spores Reveals Novel Sexual Development and Germination Factors in Cryptococcus. PLoS Genetics, 2015, 11, e1005490.	1.5	25
161	<i>Xenopus</i> CAF1 requires NOT1-mediated interaction with 4E-T to repress translation in vivo. Rna, 2015, 21, 1335-1345.	1.6	28
162	Deterministic HOX Patterning in Human Pluripotent Stem Cell-Derived Neuroectoderm. Stem Cell Reports, 2015, 4, 632-644.	2.3	162

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163	Multiplexed Quantification for Data-Independent Acquisition. Analytical Chemistry, 2015, 87, 2570-2575.	3.2	43
164	Maximal Oxidative Capacity during Exercise Is Associated with Skeletal Muscle Fuel Selection and Dynamic Changes in Mitochondrial Protein Acetylation. Cell Metabolism, 2015, 21, 468-478.	7.2	165
165	Plant-derived antifungal agent poacic acid targets Î²-1,3-glucan. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1490-7.	3.3	91
166	A Single Kinase Generates the Majority of the Secreted Phosphoproteome. Cell, 2015, 161, 1619-1632.	13.5	264
167	High-Resolution Filtering for Improved Small Molecule Identification via GC/MS. Analytical Chemistry, 2015, 87, 8328-8335.	3.2	43
168	Potential regulatory phosphorylation sites in a <i>Medicago truncatula</i> plasma membrane proton pump implicated during early symbiotic signaling in roots. FEBS Letters, 2015, 589, 2186-2193.	1.3	9
169	A role for the mevalonate pathway in early plant symbiotic signaling. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9781-9786.	3.3	111
170	Phosphorylation at the Homotypic Interface Regulates Nucleoprotein Oligomerization and Assembly of the Influenza Virus Replication Machinery. PLoS Pathogens, 2015, 11, e1004826.	2.1	53
171	A Calibration Routine for Efficient ETD in Large-Scale Proteomics. Journal of the American Society for Mass Spectrometry, 2015, 26, 1848-1857.	1.2	48
172	Metabolism of Multiple Aromatic Compounds in Corn Stover Hydrolysate by <i>Rhodopseudomonas palustris</i>. Environmental Science & Technology, 2015, 49, 8914-8922.	4.6	51
173	Serine effects on collision-induced dissociation and photodissociation of peptide cation radicals of the +â—•type. International Journal of Mass Spectrometry, 2015, 378, 20-30.	0.7	17
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