Kim K Hixson

List of Publications by Year
in descending order

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50 papers	4,200 citations	147801 31 h-index	206112 48 g-index
52 all docs	52 docs citations	52 times ranked	5741 citing authors

#	Article	IF	Citations
1	Omic data from evolved <i>E. coli</i> are consistent with computed optimal growth from genomeâ€scale models. Molecular Systems Biology, 2010, 6, 390.	7.2	615
2	Drought delays development of the sorghum root microbiome and enriches for monoderm bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4284-E4293.	7.1	391
3	Global analysis of the <i>Deinococcus radiodurans</i> proteome by using accurate mass tags. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11049-11054.	7.1	383
4	Automated 20 kpsi RPLC-MS and MS/MS with Chromatographic Peak Capacities of 1000âˆ’1500 and Capabilities in Proteomics and Metabolomics. Analytical Chemistry, 2005, 77, 3090-3100.	6.5	227
5	Ultrasensitive Proteomics Using High-Efficiency On-Line Micro-SPE-NanoLC-NanoESI MS and MS/MS. Analytical Chemistry, 2004, 76, 144-154.	6.5	188
6	Establishing the Proteome of Normal Human Cerebrospinal Fluid. PLoS ONE, 2010, 5, e10980.	2.5	183
7	Integrative Analysis of the Mitochondrial Proteome in Yeast. PLoS Biology, 2004, 2, e160.	5.6	181
8	Protein composition of the vaccinia virus mature virion. Virology, 2007, 358, 233-247.	2.4	152
9	Preparation of 20-Î¼m-i.d. Silica-Based Monolithic Columns and Their Performance for Proteomics Analyses. Analytical Chemistry, 2005, 77, 5028-5035.	6.5	137
10	The proteome of dissimilatory metal-reducing microorganism Geobacter sulfurreducens under various growth conditions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 1198-1206.	2.3	128
11	Quantitative Phosphoproteomic Analysis of Soybean Root Hairs Inoculated with Bradyrhizobium japonicum. Molecular and Cellular Proteomics, 2012, 11, 1140-1155.	3.8	126
12	Evolution and regulation of nitrogen flux through compartmentalized metabolic networks in a marine diatom. Nature Communications, 2019, 10, 4552.	12.8	116
13	Proteome of Geobacter sulfurreducens grown with Fe(III) oxide or Fe(III) citrate as the electron acceptor. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1935-1941.	2.3	113
14	High-Efficiency On-Line Solid-Phase Extraction Coupling to 15âˆ’150-Î¼m-i.d. Column Liquid Chromatography for Proteomic Analysis. Analytical Chemistry, 2003, 75, 3596-3605.	6.5	104
15	Genome Sequence of the Deltaproteobacterial Strain NaphS2 and Analysis of Differential Gene Expression during Anaerobic Growth on Naphthalene. PLoS ONE, 2010, 5, e14072.	2.5	90
16	Application of Pressurized Solvents for Ultrafast Trypsin Hydrolysis in Proteomics: Proteomics on the Fly. Journal of Proteome Research, 2008, 7, 3276-3281.	3.7	84
17	Integration of Electrokinetic-Based Multidimensional Separation/Concentration Platform with Electrospray Ionization-Fourier Transform Ion Cyclotron Resonance-Mass Spectrometry for Proteome Analysis ofShewanella oneidensis. Analytical Chemistry, 2003, 75, 4432-4440.	6.5	70
18	The state of rhizospheric science in the era of multi-omics: A practical guide to omics technologies. Rhizosphere, 2017, 3, 212-221.	3.0	66

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19	The distinct proteome of placental malaria parasites. Molecular and Biochemical Parasitology, 2007, 155, 57-65.	1.1	56
20	Soybean Roots Grown under Heat Stress Show Global Changes in Their Transcriptional and Proteomic Profiles. Frontiers in Plant Science, 2016, 7, 517.	3.6	56
21	More Sensitive and Quantitative Proteomic Measurements Using Very Low Flow Rate Porous Silica Monolithic LC Columns with Electrospray Ionization-Mass Spectrometry. Journal of Proteome Research, 2006, 5, 1091-1097.	3.7	54
22	On-line Digestion System for Protein Characterization and Proteome Analysis. Analytical Chemistry, 2008, 80, 8930-8936.	6.5	49
23	Proteome-Wide Identification of Proteins and Their Modifications with Decreased Ambiguities and Improved False Discovery Rates Using Unique Sequence Tags. Analytical Chemistry, 2008, 80, 1871-1882.	6.5	46
24	Biomarker Candidate Identification inYersiniapestisUsing Organism-Wide Semiquantitative Proteomics. Journal of Proteome Research, 2006, 5, 3008-3017.	3.7	42
25	Pressurized Pepsin Digestion in Proteomics. Molecular and Cellular Proteomics, 2011, 10, S1-S11.	3.8	41
26	Rapid Sample Processing for LC-MS-Based Quantitative Proteomics Using High Intensity Focused Ultrasound. Journal of Proteome Research, 2008, 7, 3860-3867.	3.7	40
27	High Sensitivity Proteomics Assisted Discovery of a Novel Operon Involved in the Assembly of Photosystem II, a Membrane Protein Complex. Journal of Biological Chemistry, 2008, 283, 27829-27837.	3.4	39
28	De Novo Sequencing of Unique Sequence Tags for Discovery of Post-Translational Modifications of Proteins. Analytical Chemistry, 2008, 80, 7742-7754.	6.5	36
29	Evaluation of a High-Intensity Focused Ultrasound-Immobilized Trypsin Digestion and 18O-Labeling Method for Quantitative Proteomics. Analytical Chemistry, 2009, 81, 6272-6277.	6.5	35
30	Evaluation of enzymatic digestion and liquid chromatography-mass spectrometry peptide mapping of the integral membrane protein bacteriorhodopsin. Electrophoresis, 2002, 23, 3224-3232.	2.4	34
31	Proteomic Detection of Non-Annotated Protein-Coding Genes in Pseudomonas fluorescens Pf0-1. PLoS ONE, 2009, 4, e8455.	2.5	34
32	Proteome of Geobacter sulfurreducens in the presence of U(VI). Microbiology (United Kingdom), 2014, 160, 2607-2617.	1.8	34
33	A Method to Determine Lysine Acetylation Stoichiometries. International Journal of Proteomics, 2014, 2014, 1-8.	2.0	33
34	Spatially Resolved Proteome Profiling of <200 Cells from Tomato Fruit Pericarp by Integrating Laser-Capture Microdissection with Nanodroplet Sample Preparation. Analytical Chemistry, 2018, 90, 11106-11114.	6.5	31
35	Identification of soybean proteins from a single cell type: The root hair. Proteomics, 2012, 12, 3365-3373.	2.2	29
36	Analyzing protease specificity and detecting <i>in vivo</i> proteolytic events using tandem mass spectrometry. Proteomics, 2010, 10, 2833-2844.	2.2	27

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37	Defects in the Expression of Chloroplast Proteins Leads to H2O2 Accumulation and Activation of Cyclic Electron Flow around Photosystem I. Frontiers in Plant Science, 2016, 7, 2073.	3.6	25
38	Proteomic and Physiological Responses of Kineococcus radiotolerans to Copper. PLoS ONE, 2010, 5, e12427.	2.5	19
39	Reduced Arogenate Dehydratase Expression: Ramifications for Photosynthesis and Metabolism. Plant Physiology, 2018, 177, 115-131.	4.8	18
40	Proteome Analysis of Desulfovibrio desulfuricans G20 Mutants Using the Accurate Mass and Time (AMT) Tag Approach. Journal of Proteome Research, 2007, 6, 3042-3053.	3.7	14
41	Mass Spectrometry Analysis of Proteome-Wide Proteolytic Post-Translational Degradation of Proteins. Analytical Chemistry, 2008, 80, 5819-5828.	6.5	14
42	Top-down mass spectrometry of histone modifications in sorghum reveals potential epigenetic markers for drought acclimation. Methods, 2020, 184, 29-39.	3.8	14
43	AMT Tag Approach to Proteomic Characterization ofDeinococcus radioduransandShewanella oneidensis. Methods of Biochemical Analysis, 2005, , 113-134.	0.2	4
44	Plant iTRAQâ€Based Proteomics. Current Protocols in Plant Biology, 2017, 2, 158-172.	2.8	4
45	The Importance of Protein Phosphorylation for Signaling and Metabolism in Response to Diel Light Cycling and Nutrient Availability in a Marine Diatom. Biology, 2020, 9, 155.	2.8	4
46	Multi-omic Data Integration Links Deleted in Breast Cancer 1 (DBC1) Degradation to Chromatin Remodeling in Inflammatory Response. Molecular and Cellular Proteomics, 2013, 12, 2136-2147.	3.8	3
47	Label-Free Relative Quantitation of Prokaryotic Proteomes Using the Accurate Mass and Time Tag Approach. Methods in Molecular Biology, 2009, 492, 39-63.	0.9	2
48	Ultra-Fast Sample Preparation for High-Throughput Proteomics. , 2011, , 125-139.		2
49	New Insights Into Lignification via Network and Multi-Omics Analyses of Arogenate Dehydratase Knock-Out Mutants in Arabidopsis thaliana. Frontiers in Plant Science, 2021, 12, 664250.	3.6	1
50	Deciphering the microbial and molecular responses of geographically diverse Setaria accessions grown in a nutrient-poor soil. PLoS ONE, 2021, 16, e0259937.	2.5	0