

# Leslie M Hicks

## List of Publications by Year in descending order

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98  
papers

5,294  
citations

101543

36  
h-index

88630

70  
g-index

102  
all docs

102  
docs citations

102  
times ranked

8385  
citing authors

#	ARTICLE	IF	CITATIONS
1	Selective chemical labeling reveals the genome-wide distribution of 5-hydroxymethylcytosine. <i>Nature Biotechnology</i> , 2011, 29, 68-72.	17.5	955
2	A Raf-Like MAPKKK Gene <i>DSM1</i> Mediates Drought Resistance through Reactive Oxygen Species Scavenging in Rice. <i>Plant Physiology</i> , 2010, 152, 876-890.	4.8	340
3	The response of <i>Chlamydomonas reinhardtii</i> to nitrogen deprivation: a systems biology analysis. <i>Plant Journal</i> , 2015, 81, 611-624.	5.7	207
4	Abscisic acid controls calcium-dependent egress and development in <i>Toxoplasma gondii</i> . <i>Nature</i> , 2008, 451, 207-210.	27.8	185
5	<i>In vitro</i> specificities of Arabidopsis coactivator histone acetyltransferases: implications for histone hyperacetylation in gene activation. <i>Plant Journal</i> , 2007, 52, 615-626.	5.7	181
6	Identification of Evening Complex Associated Proteins in Arabidopsis by Affinity Purification and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 201-217.	3.8	170
7	Thiol-Based Regulation of Redox-Active Glutamate-Cysteine Ligase from <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2007, 19, 2653-2661.	6.6	154
8	Protein cysteine phosphorylation of SarA/MgrA family transcriptional regulators mediates bacterial virulence and antibiotic resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15461-15466.	7.1	151
9	Comprehensive analysis of the <i>Brassica juncea</i> root proteome in response to cadmium exposure by complementary proteomic approaches. <i>Proteomics</i> , 2009, 9, 2419-2431.	2.2	148
10	A Second Target of the Antimalarial and Antibacterial Agent Fosmidomycin Revealed by Cellular Metabolic Profiling. <i>Biochemistry</i> , 2011, 50, 3570-3577.	2.5	142
11	The <i>Pseudomonas aeruginosa</i> multidrug efflux regulator MexR uses an oxidation-sensing mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13586-13591.	7.1	139
12	Divergent metabolome and proteome suggest functional independence of dual phloem transport systems in cucurbits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13532-13537.	7.1	136
13	Comprehensive Comparison of iTRAQ and Label-free LC-Based Quantitative Proteomics Approaches Using Two <i>Chlamydomonas reinhardtii</i> Strains of Interest for Biofuels Engineering. <i>Journal of Proteome Research</i> , 2012, 11, 487-501.	3.7	128
14	Proteome-wide Quantification and Characterization of Oxidation-Sensitive Cysteines in Pathogenic Bacteria. <i>Cell Host and Microbe</i> , 2013, 13, 358-370.	11.0	111
15	The Global Phosphoproteome of <i>Chlamydomonas reinhardtii</i> Reveals Complex Organellar Phosphorylation in the Flagella and Thylakoid Membrane. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2337-2353.	3.8	100
16	Identification of regulatory network hubs that control lipid metabolism in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 4551-4566.	4.8	100
17	The Regulation of Photosynthetic Structure and Function during Nitrogen Deprivation in <i>Chlamydomonas reinhardtii</i> . <i>Plant Physiology</i> , 2015, 167, 558-573.	4.8	94
18	Two Arabidopsis cytochrome P450 monooxygenases, CYP714A1 and CYP714A2, function redundantly in plant development through gibberellin deactivation. <i>Plant Journal</i> , 2011, 67, 342-353.	5.7	93

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19	Quorum-sensing <i>agr</i> mediates bacterial oxidation response via an intramolecular disulfide redox switch in the response regulator AgrA. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9095-9100.	7.1	92
20	Kinetic Basis for the Conjugation of Auxin by a GH3 Family Indole-acetic Acid-Amido Synthetase. Journal of Biological Chemistry, 2010, 285, 29780-29786.	3.4	91
21	Phosphoethanolamine N-methyltransferase (PMT-1) catalyses the first reaction of a new pathway for phosphocholine biosynthesis in <i>Caenorhabditis elegans</i> . Biochemical Journal, 2007, 404, 439-448.	3.7	69
22	Changes in protein abundance during powdery mildew infection of leaf tissues of Cabernet Sauvignon grapevine ( <i>Vitis vinifera</i> L.). Proteomics, 2010, 10, 2057-2064.	2.2	69
23	Proteomic Analysis of Early-Responsive Redox-Sensitive Proteins in <i>Arabidopsis</i> . Journal of Proteome Research, 2012, 11, 412-424.	3.7	69
24	Defining the Role of Phosphomethylethanolamine N-Methyltransferase from <i>Caenorhabditis elegans</i> in Phosphocholine Biosynthesis by Biochemical and Kinetic Analysis. Biochemistry, 2006, 45, 6056-6065.	2.5	68
25	Characterization of the Central Metabolic Pathways in <i>Thermoanaerobacter</i> sp. Strain X514 via Isotopomer-Assisted Metabolite Analysis. Applied and Environmental Microbiology, 2009, 75, 5001-5008.	3.1	57
26	From climate change to molecular response: redox proteomics of ozone-induced responses in soybean. New Phytologist, 2012, 194, 220-229.	7.3	57
27	Flexzyme-Enabled Benchtop Biosynthesis of Thiopeptides. Journal of the American Chemical Society, 2019, 141, 758-762.	13.7	56
28	Alternative isoleucine synthesis pathway in cyanobacterial species. Microbiology (United Kingdom), 2010, 156, 596-602.	1.8	52
29	Structural Characterization of in Vitro and in Vivo Intermediates on the Loading Module of Microcystin Synthetase. ACS Chemical Biology, 2006, 1, 93-102.	3.4	50
30	Investigating the effect of target of rapamycin kinase inhibition on the <i>Chlamydomonas reinhardtii</i> phosphoproteome: from known homologs to new targets. New Phytologist, 2019, 221, 247-260.	7.3	48
31	A liquid chromatography-tandem mass spectrometry-based assay for indole-3-acetic acid amido synthetase. Analytical Biochemistry, 2009, 390, 149-154.	2.4	46
32	PepSAVI-MS reveals anticancer and antifungal cycloviolacins in <i>Viola odorata</i> . Phytochemistry, 2018, 152, 61-70.	2.9	46
33	A Nucleotide Metabolite Controls Stress-Responsive Gene Expression and Plant Development. PLoS ONE, 2011, 6, e26661.	2.5	45
34	Phosphorus Availability Regulates TORC1 Signaling via LST8 in <i>Chlamydomonas</i> . Plant Cell, 2020, 32, 69-80.	6.6	43
35	Mass Spectrometric Interrogation of Thioester-Bound Intermediates in the Initial Stages of Epothilone Biosynthesis. Chemistry and Biology, 2004, 11, 327-335.	6.0	41
36	Nuclear localization of the <i>Saccharomyces cerevisiae</i> ribonucleotide reductase small subunit requires a karyopherin and a WD40 repeat protein. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1422-1427.	7.1	41

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37	ABA-Dependent and -Independent G-Protein Signaling in <i>Arabidopsis</i> Roots Revealed through an iTRAQ Proteomics Approach. <i>Journal of Proteome Research</i> , 2011, 10, 3107-3122.	3.7	38
38	Quantitative Proteomics-Based Analysis Supports a Significant Role of GTG Proteins in Regulation of ABA Response in <i>Arabidopsis</i> Roots. <i>Journal of Proteome Research</i> , 2013, 12, 1487-1501.	3.7	38
39	The "PepSAVI-MS" Pipeline for Natural Product Bioactive Peptide Discovery. <i>Analytical Chemistry</i> , 2017, 89, 1194-1201.	6.5	34
40	Contributions of conserved serine and tyrosine residues to catalysis, ligand binding, and cofactor processing in the active site of tyrosine ammonia lyase. <i>Phytochemistry</i> , 2008, 69, 1496-1506.	2.9	32
41	Redox Switching of Adenosine-5'-phosphosulfate Kinase with Photoactivatable Atomic Oxygen Precursors. <i>Journal of the American Chemical Society</i> , 2012, 134, 16979-16982.	13.7	31
42	Quantitative Proteomics Analysis of <i>Camelina sativa</i> Seeds Overexpressing the <i>AGG3</i> Gene to Identify the Proteomic Basis of Increased Yield and Stress Tolerance. <i>Journal of Proteome Research</i> , 2015, 14, 2606-2616.	3.7	30
43	Probing the global kinome and phosphoproteome in <i>Chlamydomonas reinhardtii</i> via sequential enrichment and quantitative proteomics. <i>Plant Journal</i> , 2017, 89, 416-426.	5.7	29
44	The phosphorylated redox proteome of <i>Chlamydomonas reinhardtii</i> : Revealing novel means for regulation of protein structure and function. <i>Redox Biology</i> , 2018, 17, 35-46.	9.0	29
45	Proteome-Wide Analysis of Cysteine Reactivity during Effector-Triggered Immunity. <i>Plant Physiology</i> , 2019, 179, 1248-1264.	4.8	26
46	Quantifying Reversible Oxidation of Protein Thiols in Photosynthetic Organisms. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 631-640.	2.8	25
47	Tyrosine phosphorylation switching of a G protein. <i>Journal of Biological Chemistry</i> , 2018, 293, 4752-4766.	3.4	23
48	Investigating Nonribosomal Peptide and Polyketide Biosynthesis by Direct Detection of Intermediates on >70 kDa Polypeptides by Using Fourier-Transform Mass Spectrometry. <i>ChemBioChem</i> , 2006, 7, 904-907.	2.6	21
49	Inhibition of TOR in <i>Chlamydomonas reinhardtii</i> Leads to Rapid Cysteine Oxidation Reflecting Sustained Physiological Changes. <i>Cells</i> , 2019, 8, 1171.	4.1	21
50	Contemporary mass spectrometry for the direct detection of enzyme intermediates. <i>Current Opinion in Chemical Biology</i> , 2005, 9, 424-430.	6.1	20
51	PepSAVI-MS Reveals a Proline-rich Antimicrobial Peptide in <i>Amaranthus tricolor</i> . <i>Journal of Natural Products</i> , 2019, 82, 2744-2753.	3.0	16
52	Evaluation of linear models and missing value imputation for the analysis of peptide-centric proteomics. <i>BMC Bioinformatics</i> , 2019, 20, 102.	2.6	16
53	<i>Viola</i> "inconspicua" No More: An Analysis of Antibacterial Cyclotides. <i>Journal of Natural Products</i> , 2019, 82, 2537-2543.	3.0	15
54	Maleimide-Based Chemical Proteomics for Quantitative Analysis of Cysteine Reactivity. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1697-1705.	2.8	15

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55	SVM-SulfoSite: A support vector machine based predictor for sulfenylation sites. <i>Scientific Reports</i> , 2018, 8, 11288.	3.3	14
56	Photosynthetic Metabolism and Nitrogen Reshuffling Are Regulated by Reversible Cysteine Thiol Oxidation Following Nitrogen Deprivation in <i>Chlamydomonas</i> . <i>Plants</i> , 2020, 9, 784.	3.5	14
57	Redox-regulatory mechanisms induced by oxidative stress in <i>Brassica juncea</i> roots monitored by 2D-DE proteomics. <i>Proteomics</i> , 2011, 11, 1346-1350.	2.2	13
58	Label-free quantitative proteomic analysis of pre-flowering PMeV-infected <i>Carica papaya</i> L.. <i>Journal of Proteomics</i> , 2017, 151, 275-283.	2.4	12
59	Fourier-transform mass spectrometry for detection of thioester-bound intermediates in unfractionated proteolytic mixtures of 80 and 191 kDa portions of Bacitracin A synthetase. <i>Analytica Chimica Acta</i> , 2003, 496, 217-224.	5.4	10
60	Time-dependent, glucose-regulated Arabidopsis Regulator of G-protein Signaling 1 network. <i>Current Plant Biology</i> , 2016, 5, 25-35.	4.7	10
61	Multiple Classes of Antimicrobial Peptides in <i>Amaranthus tricolor</i> Revealed by Prediction, Proteomics, and Mass Spectrometric Characterization. <i>Journal of Natural Products</i> , 2021, 84, 444-452.	3.0	10
62	A deep learning based approach for prediction of <i>Chlamydomonas reinhardtii</i> phosphorylation sites. <i>Scientific Reports</i> , 2021, 11, 12550.	3.3	10
63	Inositol polyphosphates and target of rapamycin kinase signalling govern photosystem II protein phosphorylation and photosynthetic function under light stress in <i>Chlamydomonas</i> . <i>New Phytologist</i> , 2021, 232, 2011-2025.	7.3	10
64	Implementation of Microfluidics for Antimicrobial Susceptibility Assays: Issues and Optimization Requirements. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 547177.	3.9	9
65	Leveraging orthogonal mass spectrometry based strategies for comprehensive sequencing and characterization of ribosomal antimicrobial peptide natural products. <i>Natural Product Reports</i> , 2021, 38, 489-509.	10.3	9
66	Mapping the plant proteome: tools for surveying coordinating pathways. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 203-220.	2.6	9
67	Modernizing the Analytical Chemistry Laboratory: The Design and Implementation of a Modular Protein-Centered Course. <i>Journal of Chemical Education</i> , 2021, 98, 1645-1652.	2.3	9
68	Proteomic response of <i>Escherichia coli</i> to a membrane lytic and iron chelating truncated <i>Amaranthus tricolor</i> defensin. <i>BMC Microbiology</i> , 2021, 21, 110.	3.3	9
69	Evolution of Polymyxin Resistance Regulates Colibactin Production in <i>Escherichia coli</i> . <i>ACS Chemical Biology</i> , 2021, 16, 1243-1254.	3.4	9
70	IreK-Mediated, Cell Wall-Protective Phosphorylation in <i>Enterococcus faecalis</i> . <i>Journal of Proteome Research</i> , 2021, 20, 5131-5144.	3.7	9
71	Receptor-Like Kinase Phosphorylation of Arabidopsis Heterotrimeric G-Protein $G\beta$ Subunit AtGPA1. <i>Proteomics</i> , 2019, 19, e1900265.	2.2	8
72	Multiplexing strategy for simultaneous detection of redox-, phospho- and total proteome - understanding TOR regulating pathways in <i>Chlamydomonas reinhardtii</i> . <i>Analytical Methods</i> , 2015, 7, 7336-7344.	2.7	7

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73	Fungal Secretome Analysis via PepSAVI-MS: Identification of the Bioactive Peptide KP4 from <i>Ustilago maydis</i> . <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 859-865.	2.8	7
74	Exploring bioactive peptides from bacterial secretomes using PepSAVI-MS: identification and characterization of Bac21 from <i>Enterococcus faecalis</i> pPD1. <i>Microbial Biotechnology</i> , 2018, 11, 943-951.	4.2	7
75	The Nucleotide-Dependent Interactome of Rice Heterotrimeric G-Protein $\gamma$ Subunit. <i>Proteomics</i> , 2019, 19, 1800385.	2.2	6
76	Too Hot to Handle: Antibacterial Peptides Identified in Ghost Pepper. <i>Journal of Natural Products</i> , 2021, 84, 2200-2208.	3.0	6
77	Probing Intra- versus Interchain Kinetic Preferences of L-Thr Acylation on Dimeric VibF with Mass Spectrometry. <i>Biophysical Journal</i> , 2006, 91, 2609-2619.	0.5	5
78	Gas-Phase Sequencing of Cyclotides: Introduction of Selective Ring Opening at Dehydroalanine via Ion/Ion Reaction. <i>Analytical Chemistry</i> , 2019, 91, 15608-15616.	6.5	5
79	Profiling thimet oligopeptidase-mediated proteolysis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2021, 106, 336-350.	5.7	5
80	<i>Arabidopsis</i> thimet oligopeptidases are redox-sensitive enzymes active in the local and systemic plant immune response. <i>Journal of Biological Chemistry</i> , 2021, 296, 100695.	3.4	5
81	Label-Free Quantitative Phosphoproteomics for Algae. <i>Methods in Molecular Biology</i> , 2020, 2139, 197-211.	0.9	5
82	<i>Amaranthus hypochondriacus</i> seeds as a rich source of cysteine rich bioactive peptides. <i>Food Chemistry</i> , 2022, 377, 131959.	8.2	5
83	Developing a new interdisciplinary lab course for undergraduate and graduate students: Plant cells and proteins. <i>Biochemistry and Molecular Biology Education</i> , 2007, 35, 410-415.	1.2	4
84	Inter-laboratory optimization of protein extraction, separation, and fluorescent detection of endogenous rice allergens. <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 2198-2207.	1.3	4
85	Phosphoproteomics in photosynthetic organisms. <i>Electrophoresis</i> , 2014, 35, 3441-3451.	2.4	3
86	Exploring the Diversity of Cysteine-Rich Natural Product Peptides via MS/MS Fingerprint Ions. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1833-1843.	2.8	3
87	Mass Spectrometric Identification of Antimicrobial Peptides from Medicinal Seeds. <i>Molecules</i> , 2021, 26, 7304.	3.8	3
88	Crosslinking mass spectrometry unveils novel interactions and structural distinctions in the model green alga <i>Chlamydomonas reinhardtii</i> . <i>Molecular Omics</i> , 2021, 17, 917-928.	2.8	2
89	Identification and Characterization of Bioactive Cyclotides in <i>Viola odorata</i> using PepSAVI-MS. <i>FASEB Journal</i> , 2018, 32, 530.2.	0.5	1
90	In silico prediction and mass spectrometric characterization of botanical antimicrobial peptides. <i>Methods in Enzymology</i> , 2022, 663, 157-175.	1.0	1

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91	Creating optimized peptide libraries for AMP discovery via PepSAVI-MS. <i>Methods in Enzymology</i> , 2022, 663, 41-66.	1.0	1
92	Revealing AMP mechanisms of action through resistance evolution and quantitative proteomics. <i>Methods in Enzymology</i> , 2022, 663, 259-271.	1.0	1
93	Maximizing Depth of PTM Coverage: Generating Robust MS Datasets for Computational Prediction Modeling. <i>Methods in Molecular Biology</i> , 2022, , 1-41.	0.9	1
94	Natural product bioactive peptide discovery using PepSAVI-MS. <i>FASEB Journal</i> , 2018, 32, 120.1.	0.5	0
95	Abscisic Acid Controlled Redox Proteome of <i>Arabidopsis</i> and its Regulation by Heterotrimeric G-proteins. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
96	Physical and Mechanistic Characterization of Tardigrade Cryptobiotic States in Response to Environmental Stressors. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
97	Investigating a novel role of LARP along the algal TOR pathway. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
98	Active Learning in Graduate Analytical Chemistry Courses. <i>ACS Symposium Series</i> , 0, , 65-82.	0.5	0