

# 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	Amaranthus hypochondriacus seeds as a rich source of cysteine rich bioactive peptides. Food Chemistry, 2022, 377, 131959.	8.2	5
2	In silico prediction and mass spectrometric characterization of botanical antimicrobial peptides. Methods in Enzymology, 2022, 663, 157-175.	1.0	1
3	Creating optimized peptide libraries for AMP discovery via PepSAVI-MS. Methods in Enzymology, 2022, 663, 41-66.	1.0	1
4	Revealing AMP mechanisms of action through resistance evolution and quantitative proteomics. Methods in Enzymology, 2022, 663, 259-271.	1.0	1
5	Abscisic Acid Controlled Redox Proteome of <i>Arabidopsis</i> and its Regulation by Heterotrimeric G-proteins. FASEB Journal, 2022, 36, .	0.5	0
6	Physical and Mechanistic Characterization of Tardigrade Cryptobiotic States in Response to Environmental Stressors. FASEB Journal, 2022, 36, .	0.5	0
7	Investigating a novel role of LARP along the algal TOR pathway. FASEB Journal, 2022, 36, .	0.5	0
8	Maximizing Depth of PTM Coverage: Generating Robust MS Datasets for Computational Prediction Modeling. Methods in Molecular Biology, 2022, , 1-41.	0.9	1
9	Leveraging orthogonal mass spectrometry based strategies for comprehensive sequencing and characterization of ribosomal antimicrobial peptide natural products. Natural Product Reports, 2021, 38, 489-509.	10.3	9
10	Crosslinking mass spectrometry unveils novel interactions and structural distinctions in the model green alga <i>Chlamydomonas reinhardtii</i> . Molecular Omics, 2021, 17, 917-928.	2.8	2
11	Multiple Classes of Antimicrobial Peptides in <i>Amaranthus tricolor</i> Revealed by Prediction, Proteomics, and Mass Spectrometric Characterization. Journal of Natural Products, 2021, 84, 444-452.	3.0	10
12	Profiling thimet oligopeptidase-mediated proteolysis in <i>Arabidopsis thaliana</i> . Plant Journal, 2021, 106, 336-350.	5.7	5
13	Mapping the plant proteome: tools for surveying coordinating pathways. Emerging Topics in Life Sciences, 2021, 5, 203-220.	2.6	9
14	Modernizing the Analytical Chemistry Laboratory: The Design and Implementation of a Modular Protein-Centered Course. Journal of Chemical Education, 2021, 98, 1645-1652.	2.3	9
15	Proteomic response of <i>Escherichia coli</i> to a membrane lytic and iron chelating truncated <i>Amaranthus tricolor</i> defensin. BMC Microbiology, 2021, 21, 110.	3.3	9
16	A deep learning based approach for prediction of <i>Chlamydomonas reinhardtii</i> phosphorylation sites. Scientific Reports, 2021, 11, 12550.	3.3	10
17	Evolution of Polymyxin Resistance Regulates Colibactin Production in <i>Escherichia coli</i> . ACS Chemical Biology, 2021, 16, 1243-1254.	3.4	9
18	Too Hot to Handle: Antibacterial Peptides Identified in Ghost Pepper. Journal of Natural Products, 2021, 84, 2200-2208.	3.0	6

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19	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
20	Arabidopsis 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
21	IreK-Mediated, Cell Wall-Protective Phosphorylation in <i>Enterococcus faecalis</i> . <i>Journal of Proteome Research</i> , 2021, 20, 5131-5144.	3.7	9
22	Mass Spectrometric Identification of Antimicrobial Peptides from Medicinal Seeds. <i>Molecules</i> , 2021, 26, 7304.	3.8	3
23	Phosphorus Availability Regulates TORC1 Signaling via LST8 in <i>Chlamydomonas</i> . <i>Plant Cell</i> , 2020, 32, 69-80.	6.6	43
24	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
25	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
26	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
27	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
28	Label-Free Quantitative Phosphoproteomics for Algae. <i>Methods in Molecular Biology</i> , 2020, 2139, 197-211.	0.9	5
29	Investigating the effect of target of rapamycin kinase inhibition on the <i>Chlamydomonas reinhardtii</i> phosphoproteome: from known homologs to new targets. <i>New Phytologist</i> , 2019, 221, 247-260.	7.3	48
30	Receptor-Like Kinase Phosphorylation of Arabidopsis Heterotrimeric G-Protein $\beta$ -Subunit AtGPA1. <i>Proteomics</i> , 2019, 19, e1900265.	2.2	8
31	<i>Viola</i> <i>inconspicua</i> No More: An Analysis of Antibacterial Cyclotides. <i>Journal of Natural Products</i> , 2019, 82, 2537-2543.	3.0	15
32	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
33	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
34	The Nucleotide-Dependent Interactome of Rice Heterotrimeric G-Protein $\beta$ -Subunit. <i>Proteomics</i> , 2019, 19, 1800385.	2.2	6
35	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
36	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

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37	Flexizyme-Enabled Benchtop Biosynthesis of Thiopeptides. <i>Journal of the American Chemical Society</i> , 2019, 141, 758-762.	13.7	56
38	Proteome-Wide Analysis of Cysteine Reactivity during Effector-Triggered Immunity. <i>Plant Physiology</i> , 2019, 179, 1248-1264.	4.8	26
39	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
40	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
41	Tyrosine phosphorylation switching of a G protein. <i>Journal of Biological Chemistry</i> , 2018, 293, 4752-4766.	3.4	23
42	PepSAVI-MS reveals anticancer and antifungal cycloviolacins in <i>Viola odorata</i> . <i>Phytochemistry</i> , 2018, 152, 61-70.	2.9	46
43	SVM-SulfoSite: A support vector machine based predictor for sulfenylation sites. <i>Scientific Reports</i> , 2018, 8, 11288.	3.3	14
44	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
45	Natural product bioactive peptide discovery using PepSAVI-MS. <i>FASEB Journal</i> , 2018, 32, 120.1.	0.5	0
46	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
47	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
48	The PepSAVI-MS Pipeline for Natural Product Bioactive Peptide Discovery. <i>Analytical Chemistry</i> , 2017, 89, 1194-1201.	6.5	34
49	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
50	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
51	Time-dependent, glucose-regulated Arabidopsis Regulator of G-protein Signaling 1 network. <i>Current Plant Biology</i> , 2016, 5, 25-35.	4.7	10
52	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
53	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
54	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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55	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
56	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
57	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
58	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
59	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
60	Phosphoproteomics in photosynthetic organisms. <i>Electrophoresis</i> , 2014, 35, 3441-3451.	2.4	3
61	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
62	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
63	Quorum-sensing <i>agr</i> mediates bacterial oxidation response via an intramolecular disulfide redox switch in the response regulator AgrA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9095-9100.	7.1	92
64	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
65	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
66	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
67	Proteomic Analysis of Early-Responsive Redox-Sensitive Proteins in <i>Arabidopsis</i> . <i>Journal of Proteome Research</i> , 2012, 11, 412-424.	3.7	69
68	From climate change to molecular response: redox proteomics of ozone-induced responses in soybean. <i>New Phytologist</i> , 2012, 194, 220-229.	7.3	57
69	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
70	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
71	A Nucleotide Metabolite Controls Stress-Responsive Gene Expression and Plant Development. <i>PLoS ONE</i> , 2011, 6, e26661.	2.5	45
72	Two <i>Arabidopsis</i> 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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73	Selective chemical labeling reveals the genome-wide distribution of 5-hydroxymethylcytosine. <i>Nature Biotechnology</i> , 2011, 29, 68-72.	17.5	955
74	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
75	Changes in protein abundance during powdery mildew infection of leaf tissues of Cabernet Sauvignon grapevine ( <i>Vitis vinifera</i> L.). <i>Proteomics</i> , 2010, 10, 2057-2064.	2.2	69
76	Kinetic Basis for the Conjugation of Auxin by a GH3 Family Indole-acetic Acid-Amido Synthetase. <i>Journal of Biological Chemistry</i> , 2010, 285, 29780-29786.	3.4	91
77	Alternative isoleucine synthesis pathway in cyanobacterial species. <i>Microbiology (United Kingdom)</i> , 2010, 156, 596-602.	1.8	52
78	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
79	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
80	Characterization of the Central Metabolic Pathways in <i>Thermoanaerobacter</i> sp. Strain X514 via Isotopomer-Assisted Metabolite Analysis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5001-5008.	3.1	57
81	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
82	A liquid chromatography-tandem mass spectrometry-based assay for indole-3-acetic acid-amido synthetase. <i>Analytical Biochemistry</i> , 2009, 390, 149-154.	2.4	46
83	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
84	Abscisic acid controls calcium-dependent egress and development in <i>Toxoplasma gondii</i> . <i>Nature</i> , 2008, 451, 207-210.	27.8	185
85	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
86	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
87	Phosphoethanolamine N-methyltransferase (PMT-1) catalyses the first reaction of a new pathway for phosphocholine biosynthesis in <i>Caenorhabditis elegans</i> . <i>Biochemical Journal</i> , 2007, 404, 439-448.	3.7	69
88	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
89	<i>In vitro</i> specificities of <i>Arabidopsis</i> coactivator histone acetyltransferases: implications for histone hyperacetylation in gene activation. <i>Plant Journal</i> , 2007, 52, 615-626.	5.7	181
90	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

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91	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
92	Defining the Role of PhosphomethylethanolamineN-Methyltransferase fromCaenorhabditis elegansin Phosphocholine Biosynthesis by Biochemical and Kinetic Analysis. Biochemistry, 2006, 45, 6056-6065.	2.5	68
93	Investigating Nonribosomal Peptide and Polyketide Biosynthesis by Direct Detection of Intermediates on >70 kDa Polypeptides by Using Fourier-Transform Mass Spectrometry. ChemBioChem, 2006, 7, 904-907.	2.6	21
94	Nuclear localization of the Saccharomyces cerevisiae 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
95	Contemporary mass spectrometry for the direct detection of enzyme intermediates. Current Opinion in Chemical Biology, 2005, 9, 424-430.	6.1	20
96	Mass Spectrometric Interrogation of Thioester-Bound Intermediates in the Initial Stages of Epothilone Biosynthesis. Chemistry and Biology, 2004, 11, 327-335.	6.0	41
97	Fourier-transform mass spectrometry for detection of thioester-bound intermediates in unfractionated proteolytic mixtures of 80 and 191 kDa portions of Bacitracin A synthetase. Analytica Chimica Acta, 2003, 496, 217-224.	5.4	10
98	Active Learning in Graduate Analytical Chemistry Courses. ACS Symposium Series, 0, , 65-82.	0.5	0