

Henry Lam

List of Publications by Year in descending order

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87
papers

8,596
citations

109264

35
h-index

54882

84
g-index

91
all docs

91
docs citations

91
times ranked

12107
citing authors

#	ARTICLE	IF	CITATIONS
1	Common Decoy Distributions Simplify False Discovery Rate Estimation in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 339-348.	1.8	5
2	Proteomics and Transcriptomics Uncover Key Processes for Elasin Tolerance in Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MSystems</i> , 2022, 7, e0139321.	1.7	4
3	Proteomics in antibiotic resistance and tolerance research: Mapping the resistome and the tolerome of bacterial pathogens. <i>Proteomics</i> , 2022, 22, e2100409.	1.3	5
4	Elasin Effectively Eradicates Daptomycin-Resistant Methicillin-Resistant <i>Staphylococcus aureus</i> Biofilms. <i>Microbiology Spectrum</i> , 2022, 10, e0232021.	1.2	2
5	Fritted tip capillary column with negligible dead volume facilitated ultrasensitive and deep proteomics. <i>Analytica Chimica Acta</i> , 2022, 1201, 339615.	2.6	5
6	Quantitative Proteomics Reveals UGA-Independent Misincorporation of Selenocysteine throughout the <i>Escherichia coli</i> Proteome. <i>Journal of Proteome Research</i> , 2021, 20, 212-221.	1.8	8
7	Evolution of Bacterial Tolerance Under Antibiotic Treatment and Its Implications on the Development of Resistance. <i>Frontiers in Microbiology</i> , 2021, 12, 617412.	1.5	43
8	The Osteogenic Function of Danggui Buxue Tang, a Herbal Decoction Containing <i>Astragali Radix</i> and <i>Angelicae Sinensis Radix</i> , Is Optimized by Boiling the Two Herbs Together: Signaling Analyses Revealed by Systems Biology. <i>Processes</i> , 2021, 9, 1119.	1.3	0
9	Susceptibility to false discovery in biomarker research using liquid chromatography–high resolution mass spectrometry based untargeted metabolomics profiling. <i>Clinical and Translational Medicine</i> , 2021, 11, e469.	1.7	4
10	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021, 18, 768-770.	9.0	47
11	Integrated Omics Reveals the Orchestrating Role of Calycosin in Danggui Buxue Tang, a Herbal Formula Containing <i>Angelicae Sinensis Radix</i> and <i>Astragali Radix</i> , in Inducing Osteoblastic Differentiation and Proliferation. <i>Frontiers in Pharmacology</i> , 2021, 12, 670947.	1.6	4
12	Combinatory strategy using nanoscale proteomics and machine learning for T cell subtyping in peripheral blood of single multiple myeloma patients. <i>Analytica Chimica Acta</i> , 2021, 1173, 338672.	2.6	6
13	Comparative proteomic investigation of multiple methicillin-resistant <i>Staphylococcus aureus</i> strains generated through adaptive laboratory evolution. <i>IScience</i> , 2021, 24, 102950.	1.9	10
14	Novel Daptomycin Tolerance and Resistance Mutations in Methicillin-Resistant <i>Staphylococcus aureus</i> from Adaptive Laboratory Evolution. <i>MSphere</i> , 2021, 6, e0069221.	1.3	11
15	Mass spectrometry-based multi-omics analysis reveals the thermogenetic regulation of herbal medicine in rat model of yeast-induced fever. <i>Journal of Ethnopharmacology</i> , 2021, 279, 114382.	2.0	1
16	ClusterSheep: A Graphics Processing Unit-Accelerated Software Tool for Large-Scale Clustering of Tandem Mass Spectra from Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2021, 20, 5359-5367.	1.8	2
17	Boosting Cyanobacteria Growth by Fivefold with Aggregation-Induced Emission Luminogens: Toward the Development of a Biofactory. <i>ACS Sustainable Chemistry and Engineering</i> , 2021, 9, 15258-15266.	3.2	9
18	Proteomic analysis of thioproline misincorporation in <i>Escherichia coli</i> . <i>Journal of Proteomics</i> , 2020, 210, 103541.	1.2	11

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19	Proteomic Investigation of Tolerant <i>Escherichia coli</i> Populations from Cyclic Antibiotic Treatment. <i>Journal of Proteome Research</i> , 2020, 19, 900-913.	1.8	39
20	DPHL: A DIA Pan-human Protein Mass Spectrometry Library for Robust Biomarker Discovery. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 104-119.	3.0	51
21	Proteomic Study of the Survival and Resuscitation Mechanisms of Filamentous Persisters in an Evolved <i>Escherichia coli</i> Population from Cyclic Ampicillin Treatment. <i>MSystems</i> , 2020, 5, .	1.7	23
22	Proteomics Study of DNA-Protein Crosslinks in Methylmethanesulfonate and Fe ²⁺ -EDTA-Exposed Human Cells. <i>Chemical Research in Toxicology</i> , 2020, 33, 2739-2744.	1.7	5
23	In Vitro Salivary Protein Adsorption Profile on Titanium and Ceramic Surfaces and the Corresponding Putative Immunological Implications. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3083.	1.8	8
24	Application of proteomics in studying bacterial persistence. <i>Expert Review of Proteomics</i> , 2019, 16, 227-239.	1.3	20
25	Proteomic Analysis of Nucleus Pulposus Cell-derived Extracellular Matrix Niche and Its Effect on Phenotypic Alteration of Dermal Fibroblasts. <i>Scientific Reports</i> , 2018, 8, 1512.	1.6	14
26	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	1.8	47
27	Specific Enrichment and Proteomics Analysis of <i>Escherichia coli</i> Persisters from Rifampin Pretreatment. <i>Journal of Proteome Research</i> , 2018, 17, 3984-3996.	1.8	47
28	ABRF Proteome Informatics Research Group (iPRG) 2016 Study: Inferring Proteoforms from Bottom-up Proteomics Data. <i>Journal of Biomolecular Techniques</i> , 2018, 29, 39-45.	0.8	6
29	ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of Differentially Abundant Proteins in Label-Free Quantitative LC-MS/MS Experiments. <i>Journal of Proteome Research</i> , 2017, 16, 945-957.	1.8	42
30	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017, 16, 4288-4298.	1.8	87
31	Tandem mass spectral libraries of peptides and their roles in proteomics research. <i>Mass Spectrometry Reviews</i> , 2017, 36, 634-648.	2.8	44
32	A hybrid retention time alignment algorithm for SWATH-MS data. <i>Proteomics</i> , 2016, 16, 2272-2283.	1.3	8
33	Spectral Library Searching To Identify Cross-Linked Peptides. <i>Journal of Proteome Research</i> , 2016, 15, 1725-1731.	1.8	12
34	Direct glycan structure determination of intact N-linked glycopeptides by low-energy collision-induced dissociation tandem mass spectrometry and predicted spectral library searching. <i>Analytica Chimica Acta</i> , 2016, 934, 152-162.	2.6	21
35	Human SRMATlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. <i>Cell</i> , 2016, 166, 766-778.	13.5	295
36	Proteomic response of methicillin-resistant <i>S. aureus</i> to a synergistic antibacterial drug combination: a novel erythromycin derivative and oxacillin. <i>Scientific Reports</i> , 2016, 6, 19841.	1.6	29

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37	A peptide identification-free, genome sequence-independent shotgun proteomics workflow for strain-level bacterial differentiation. <i>Scientific Reports</i> , 2015, 5, 14337.	1.6	10
38	Fruit of <i>Ziziphus jujuba</i> (Jujube) at Two Stages of Maturity: Distinction by Metabolic Profiling and Biological Assessment. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 739-744.	2.4	28
39	Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , 2015, 10, 426-441.	5.5	319
40	An open-source computational and data resource to analyze digital maps of immunopeptidomes. <i>ELife</i> , 2015, 4, .	2.8	107
41	Metabonomic Analysis of Water Extracts from Different Angelica Roots by 1H-Nuclear Magnetic Resonance Spectroscopy. <i>Molecules</i> , 2014, 19, 3460-3470.	1.7	14
42	Quality Control of Danggui Buxue Tang, a Traditional Chinese Medicine Decoction, by H-NMR Metabolic Profiling. <i>Evidence-based Complementary and Alternative Medicine</i> , 2014, 2014, 1-8.	0.5	18
43	A draft map of the human proteome. <i>Nature</i> , 2014, 509, 575-581.	13.7	1,948
44	Label-Free Quantitative Proteomics Analysis of Antibiotic Response in <i>Staphylococcus aureus</i> to Oxacillin. <i>Journal of Proteome Research</i> , 2014, 13, 1223-1233.	1.8	71
45	Proteome Informatics Research Group (iPRG)_2012: A Study on Detecting Modified Peptides in a Complex Mixture. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 360-371.	2.5	20
46	Hunting for Unexpected Post-Translational Modifications by Spectral Library Searching with Tier-Wise Scoring. <i>Journal of Proteome Research</i> , 2014, 13, 2262-2271.	1.8	35
47	Tracking the sources of blood meals of parasitic arthropods using shotgun proteomics and unidentified tandem mass spectral libraries. <i>Nature Protocols</i> , 2014, 9, 842-850.	5.5	15
48	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031.	2.4	370
49	A High-Resolution LC-MS-Based Secondary Metabolite Fingerprint Database of Marine Bacteria. <i>Scientific Reports</i> , 2014, 4, 6537.	1.6	17
50	Chemical changes of <i>Angelicae Sinensis Radix</i> and <i>Chuanxiong Rhizoma</i> by wine treatment: chemical profiling and marker selection by gas chromatography coupled with triple quadrupole mass spectrometry. <i>Chinese Medicine</i> , 2013, 8, 12.	1.6	11
51	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. <i>Nature</i> , 2013, 494, 266-270.	13.7	307
52	Identifying sources of tick blood meals using unidentified tandem mass spectral libraries. <i>Nature Communications</i> , 2013, 4, 1746.	5.8	46
53	Denosing Peptide Tandem Mass Spectra for Spectral Libraries: A Bayesian Approach. <i>Journal of Proteome Research</i> , 2013, 12, 3223-3232.	1.8	7
54	Expanding Tandem Mass Spectral Libraries of Phosphorylated Peptides: Advances and Applications. <i>Journal of Proteome Research</i> , 2013, 12, 5971-5977.	1.8	21

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55	Stable Isotope Metabolic Labeling-based Quantitative Phosphoproteomic Analysis of Arabidopsis Mutants Reveals Ethylene-regulated Time-dependent Phosphoproteins and Putative Substrates of Constitutive Triple Response 1 Kinase. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3559-3582.	2.5	58
56	Graph-based peak alignment algorithms for multiple liquid chromatography-mass spectrometry datasets. <i>Bioinformatics</i> , 2013, 29, 2469-2476.	1.8	9
57	Refining similarity scoring to enable decoy-free validation in spectral library searching. <i>Proteomics</i> , 2013, 13, 3273-3283.	1.3	23
58	Multi-resolution LC-MS images alignment using dynamic time warping and Kullback-Leibler distance. , 2012, , .		2
59	Metabonomic analysis of water extracts from Chinese and American ginsengs by ¹ H nuclear magnetic resonance: identification of chemical profile for quality control. <i>Chinese Medicine</i> , 2012, 7, 25.	1.6	8
60	Spectral library searching for peptide identification in proteomics. <i>Statistics and Its Interface</i> , 2012, 5, 39-46.	0.2	1
61	iProphet: Multi-level Integrative Analysis of Shotgun Proteomic Data Improves Peptide and Protein Identification Rates and Error Estimates. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.007690.	2.5	490
62	Fast Parallel Tandem Mass Spectral Library Searching Using GPU Hardware Acceleration. <i>Journal of Proteome Research</i> , 2011, 10, 2882-2888.	1.8	47
63	Absolute quantification of microbial proteomes at different states by directed mass spectrometry. <i>Molecular Systems Biology</i> , 2011, 7, 510.	3.2	91
64	Building and searching tandem mass (MS/MS) spectral libraries for peptide identification in proteomics. <i>Methods</i> , 2011, 54, 424-431.	1.9	45
65	Understanding the improved sensitivity of spectral library searching over sequence database searching in proteomics data analysis. <i>Proteomics</i> , 2011, 11, 1075-1085.	1.3	64
66	A semi-empirical approach for predicting unobserved peptide MS/MS spectra from spectral libraries. <i>Proteomics</i> , 2011, 11, 4702-4711.	1.3	17
67	Building and Searching Tandem Mass Spectral Libraries for Peptide Identification. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R111.008565.	2.5	59
68	Spectral archives: a vision for future proteomics data repositories. <i>Nature Methods</i> , 2011, 8, 546-548.	9.0	8
69	A guided tour of the Trans-Proteomic Pipeline. <i>Proteomics</i> , 2010, 10, 1150-1159.	1.3	710
70	Trans-Proteomic Pipeline supports and improves analysis of electron transfer dissociation data sets. <i>Proteomics</i> , 2010, 10, 1190-1195.	1.3	39
71	A ubiquitin and ubiquitin-like protein spectral library. <i>Proteomics</i> , 2010, 10, 337-342.	1.3	17
72	Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. <i>Science Signaling</i> , 2010, 3, rs4.	1.6	277

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73	Using Spectral Libraries for Peptide Identification from Tandem Mass Spectrometry (MS/MS) Data. <i>Current Protocols in Protein Science</i> , 2010, 60, Unit 25.5.	2.8	11
74	Artificial Decoy Spectral Libraries for False Discovery Rate Estimation in Spectral Library Searching in Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 605-610.	1.8	106
75	Spectral Library Searching for Peptide Identification via Tandem MS. <i>Methods in Molecular Biology</i> , 2010, 604, 95-103.	0.4	17
76	MaRiMba: A Software Application for Spectral Library-Based MRM Transition List Assembly. <i>Journal of Proteome Research</i> , 2009, 8, 4396-4405.	1.8	80
77	PeptideAtlas: a resource for target selection for emerging targeted proteomics workflows. <i>EMBO Reports</i> , 2008, 9, 429-434.	2.0	516
78	PhosphoPep—a database of protein phosphorylation sites in model organisms. <i>Nature Biotechnology</i> , 2008, 26, 1339-1340.	9.4	192
79	Building consensus spectral libraries for peptide identification in proteomics. <i>Nature Methods</i> , 2008, 5, 873-875.	9.0	255
80	A database of mass spectrometric assays for the yeast proteome. <i>Nature Methods</i> , 2008, 5, 913-914.	9.0	205
81	Data analysis and bioinformatics tools for tandem mass spectrometry in proteomics. <i>Physiological Genomics</i> , 2008, 33, 18-25.	1.0	137
82	Development and validation of a spectral library searching method for peptide identification from MS/MS. <i>Proteomics</i> , 2007, 7, 655-667.	1.3	487
83	PhosphoPep—a phosphoproteome resource for systems biology research in <i>Drosophila</i> Kc167 cells. <i>Molecular Systems Biology</i> , 2007, 3, 139.	3.2	168
84	Affinity-tagged green fluorescent protein (GFP) extraction from a clarified <i>E. coli</i> cell lysate using a two-phase aqueous micellar system. <i>Biotechnology and Bioengineering</i> , 2006, 93, 998-1004.	1.7	29
85	Affinity-enhanced protein partitioning in decyl β -D-glucopyranoside two-phase aqueous micellar systems. <i>Biotechnology and Bioengineering</i> , 2005, 89, 381-392.	1.7	36
86	Glucose-6-phosphate dehydrogenase partitioning in two-phase aqueous mixed (nonionic/cationic) micellar systems. <i>Biotechnology and Bioengineering</i> , 2003, 82, 445-456.	1.7	44
87	Proteomics-Based Elucidation of Natural Product Biosynthetic Pathways in <i>Streptomyces</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1