

Hookeun Lee

List of Publications by Year in descending order

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107
papers

5,057
citations

94381

37
h-index

91828

69
g-index

107
all docs

107
docs citations

107
times ranked

6512
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational prediction of proteotypic peptides for quantitative proteomics. <i>Nature Biotechnology</i> , 2007, 25, 125-131.	9.4	653
2	Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry. <i>Genome Biology</i> , 2004, 6, R9.	13.9	252
3	A high-quality catalog of the <i>Drosophila melanogaster</i> proteome. <i>Nature Biotechnology</i> , 2007, 25, 576-583.	9.4	247
4	Approaching complete peroxisome characterization by gas-phase fractionation. <i>Electrophoresis</i> , 2002, 23, 3205-3216.	1.3	193
5	Proteogenomic Characterization of Human Early-Onset Gastric Cancer. <i>Cancer Cell</i> , 2019, 35, 111-124.e10.	7.7	183
6	Gene Expression Analyzed by High-resolution State Array Analysis and Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 478-489.	2.5	178
7	Proteome Analysis of <i>Legionella</i> Vacuoles Purified by Magnetic Immunoseparation Reveals Secretory and Endosomal GTPases. <i>Traffic</i> , 2009, 10, 76-87.	1.3	163
8	The Standard Protein Mix Database: A Diverse Data Set To Assist in the Production of Improved Peptide and Protein Identification Software Tools. <i>Journal of Proteome Research</i> , 2008, 7, 96-103.	1.8	156
9	Human Plasma PeptideAtlas. <i>Proteomics</i> , 2005, 5, 3497-3500.	1.3	132
10	Increased quantitative proteome coverage with ¹³ C/ ¹² C-based, acid-cleavable isotope-coded affinity tag reagent and modified data acquisition scheme. <i>Proteomics</i> , 2005, 5, 380-387.	1.3	118
11	Signal Maps for Mass Spectrometry-based Comparative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 423-432.	2.5	110
12	A microcapillary trap cartridge-microcapillary high-performance liquid chromatography electrospray ionization emitter device capable of peptide tandem mass spectrometry at the attomole level on an ion trap mass spectrometer with automated routine operation. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 2093-2098.	0.7	101
13	UniPep—a database for human N-linked glycosites: a resource for biomarker discovery. <i>Genome Biology</i> , 2006, 7, R73.	13.9	101
14	Quantitative Proteomic Analysis of Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 326-346.	2.5	99
15	Advances in proteomic workflows for systems biology. <i>Current Opinion in Biotechnology</i> , 2007, 18, 378-384.	3.3	95
16	Toward a high-throughput approach to quantitative proteomic analysis: Expression-dependent protein identification by mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 1238-1246.	1.2	93
17	A Small Molecule That Binds to an ATPase Domain of Hsc70 Promotes Membrane Trafficking of Mutant Cystic Fibrosis Transmembrane Conductance Regulator. <i>Journal of the American Chemical Society</i> , 2011, 133, 20267-20276.	6.6	93
18	A Tool To Visualize and Evaluate Data Obtained by Liquid Chromatography-Electrospray Ionization-Mass Spectrometry. <i>Analytical Chemistry</i> , 2004, 76, 3856-3860.	3.2	88

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19	Optimized Peptide Separation and Identification for Mass Spectrometry Based Proteomics via Free-Flow Electrophoresis. <i>Journal of Proteome Research</i> , 2006, 5, 2241-2249.	1.8	88
20	Analysis of Whole Bacterial Cells by Flow Field-Flow Fractionation and Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 2746-2752.	3.2	81
21	Quantitative Proteomic Analysis of Metabolic Regulation by Copper Ions in <i>Methylococcus capsulatus</i> (Bath). <i>Journal of Biological Chemistry</i> , 2004, 279, 51554-51560.	1.6	80
22	Proteomic Identification of Potential Susceptibility Factors in Drug-Induced Liver Disease. <i>Chemical Research in Toxicology</i> , 2005, 18, 924-933.	1.7	75
23	Analysis of Self-Assembled Cationic Lipid-DNA Gene Carrier Complexes Using Flow Field-Flow Fractionation and Light Scattering. <i>Analytical Chemistry</i> , 2001, 73, 837-843.	3.2	74
24	Quantitative Proteomic Analysis of Myc-induced Apoptosis. <i>Journal of Biological Chemistry</i> , 2006, 281, 2750-2756.	1.6	65
25	System-based proteomic analysis of the interferon response in human liver cells. <i>Genome Biology</i> , 2004, 5, R54.	13.9	63
26	Abundance Ratio-Dependent Proteomic Analysis by Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 867-874.	3.2	62
27	Analysis of the <i>Saccharomyces cerevisiae</i> proteome with PeptideAtlas. <i>Genome Biology</i> , 2006, 7, R106.	13.9	60
28	A Dataset of Human Liver Proteins Identified by Protein Profiling Via Isotope-coded Affinity Tag (ICAT) and Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 1039-1041.	2.5	56
29	Development of a Multiplexed Microcapillary Liquid Chromatography System for High-Throughput Proteome Analysis. <i>Analytical Chemistry</i> , 2002, 74, 4353-4360.	3.2	55
30	Effects of Light Intensity and Nitrogen Starvation on Glycerolipid, Glycerophospholipid, and Carotenoid Composition in <i>Dunaliella tertiolecta</i> Culture. <i>PLoS ONE</i> , 2013, 8, e72415.	1.1	53
31	Assessing Bias in Experiment Design for Large Scale Mass Spectrometry-based Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1741-1748.	2.5	52
32	Elucidation of the growth delimitation of <i>Dunaliella tertiolecta</i> under nitrogen stress by integrating transcriptome and peptidome analysis. <i>Bioresource Technology</i> , 2015, 194, 57-66.	4.8	51
33	Review of Three-Dimensional Liquid Chromatography Platforms for Bottom-Up Proteomics. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1524.	1.8	50
34	Proteomic Analysis of Serum from Patients with Major Depressive Disorder to Compare Their Depressive and Remission Statuses. <i>Psychiatry Investigation</i> , 2015, 12, 249.	0.7	44
35	The toposome, essential for sea urchin cell adhesion and development, is a modified iron-less calcium-binding transferrin. <i>Developmental Biology</i> , 2007, 310, 54-70.	0.9	39
36	Protein Expression Changes in Ovarian Cancer during the Transition from Benign to Malignant. <i>Journal of Proteome Research</i> , 2012, 11, 2876-2889.	1.8	39

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37	Fatty acids and global metabolites profiling of <i>Dunaliella tertiolecta</i> by shifting culture conditions to nitrate deficiency and high light at different growth phases. <i>Process Biochemistry</i> , 2014, 49, 996-1004.	1.8	39
38	Quantitative proteomic analysis of the budding yeast cell cycle using acid-cleavable isotope-coded affinity tag reagents. <i>Proteomics</i> , 2006, 6, 6146-6157.	1.3	38
39	Genome-wide transcriptome analysis revealed organelle specific responses to temperature variations in algae. <i>Scientific Reports</i> , 2016, 6, 37770.	1.6	38
40	Label-free quantification for discovering novel biomarkers in the diagnosis and assessment of disease activity in inflammatory bowel disease. <i>Journal of Digestive Diseases</i> , 2013, 14, 166-174.	0.7	37
41	Effect of Ethephon as an Ethylene-Releasing Compound on the Metabolic Profile of <i>Chlorella vulgaris</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 4807-4816.	2.4	37
42	Evaluation of Different Field-Flow Fractionation Techniques for Separating Bacteria. <i>Separation Science and Technology</i> , 2000, 35, 1761-1775.	1.3	35
43	Integrated analysis of global proteome, phosphoproteome and glycoproteome enables complementary interpretation of disease-related protein networks. <i>Scientific Reports</i> , 2015, 5, 18189.	1.6	34
44	Optimization of reversed-phase microcapillary liquid chromatography for quantitative proteomics. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2004, 803, 101-110.	1.2	32
45	Particle Size Analysis of Dilute Environmental Colloids by Flow Field-Flow Fractionation Using an Opposed Flow Sample Concentration Technique. <i>Analytical Chemistry</i> , 1998, 70, 2495-2503.	3.2	29
46	Ultrasmall gold nanoparticles for highly specific isolation/enrichment of N-linked glycosylated peptides. <i>Analyst</i> , 2012, 137, 991-998.	1.7	28
47	Atorvastatin and Simvastatin, but not Pravastatin, Up-regulate LPS-Induced MMP-9 Expression in Macrophages by Regulating Phosphorylation of ERK and CREB. <i>Cellular Physiology and Biochemistry</i> , 2012, 30, 499-511.	1.1	27
48	Integrated Post-Experiment Monoisotopic Mass Refinement: An Integrated Approach to Accurately Assign Monoisotopic Precursor Masses to Tandem Mass Spectrometric Data. <i>Analytical Chemistry</i> , 2010, 82, 8510-8518.	3.2	21
49	Current Status and Future Strategies to Increase Secondary Metabolite Production from Cyanobacteria. <i>Microorganisms</i> , 2020, 8, 1849.	1.6	21
50	Proteomics in Forensic Analysis: Applications for Human Samples. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 3393.	1.3	21
51	Dihydrolipoyl dehydrogenase as a potential UVB target in skin epidermis; using an integrated approach of label-free quantitative proteomics and targeted metabolite analysis. <i>Journal of Proteomics</i> , 2015, 117, 70-85.	1.2	20
52	Effects of FGF2-secreting adipose-derived stem cells in thioacetamide-induced hepatic fibrosis. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 5165-5169.	1.6	19
53	Discovery of plasma biomarkers for predicting the severity of coronary artery atherosclerosis by quantitative proteomics. <i>BMJ Open Diabetes Research and Care</i> , 2020, 8, e001152.	1.2	19
54	Neural Ganglia Transcriptome and Peptidome Associated with Sexual Maturation in Female Pacific Abalone (<i>Haliotis discus hannai</i>). <i>Genes</i> , 2019, 10, 268.	1.0	18

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55	Establishment of functional epithelial organoids from human lacrimal glands. <i>Stem Cell Research and Therapy</i> , 2021, 12, 247.	2.4	18
56	Combining selected reaction monitoring with discovery proteomics in limited biological samples. <i>Proteomics</i> , 2009, 9, 4834-4836.	1.3	17
57	Size characterization of magnetic cell sorting microbeads using flow field-flow fractionation and photon correlation spectroscopy. <i>Journal of Magnetism and Magnetic Materials</i> , 1999, 194, 248-253.	1.0	16
58	Preventive effect of <i>Rhus javanica</i> extract on UVB-induced skin inflammation and photoaging. <i>Journal of Functional Foods</i> , 2016, 27, 589-599.	1.6	16
59	Photosynthetic pigment production and metabolic and lipidomic alterations in the marine cyanobacteria <i>Synechocystis</i> sp. PCC 7338 under various salinity conditions. <i>Journal of Applied Phycology</i> , 2021, 33, 197-209.	1.5	16
60	Efficient protein digestion using highly-stable and reproducible trypsin coatings on magnetic nanofibers. <i>Chemical Engineering Journal</i> , 2016, 288, 770-777.	6.6	15
61	Proteome Analysis of <i>Halobacterium</i> sp. NRC-1 Facilitated by the Biomodule Analysis Tool BMSorter. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 987-997.	2.5	14
62	The effect and potential of using a temperature controlled separation column with ultra-high pressure microcapillary liquid chromatography/tandem mass spectrometry on proteomic analysis. <i>Analyst</i> , The, 2011, 136, 2100.	1.7	14
63	Enhanced production of fatty acids in three strains of microalgae using a combination of nitrogen starvation and chemical inhibitors of carbohydrate synthesis. <i>Biotechnology and Bioprocess Engineering</i> , 2017, 22, 60-67.	1.4	14
64	MS-BID: a Java package for label-free LC-MS-based comparative proteomic analysis. <i>Bioinformatics</i> , 2008, 24, 2641-2642.	1.8	12
65	Development of an Automated, High-throughput Sample Preparation Protocol for Proteomics Analysis. <i>Bulletin of the Korean Chemical Society</i> , 2015, 36, 1791-1798.	1.0	12
66	UBA2 activates Wnt/ β -catenin signaling pathway during protection of R28 retinal precursor cells from hypoxia by extracellular vesicles derived from placental mesenchymal stem cells. <i>Stem Cell Research and Therapy</i> , 2020, 11, 428.	2.4	12
67	Externalized phosphatidylinositides on apoptotic cells are eat-me signals recognized by CD14. <i>Cell Death and Differentiation</i> , 2022, 29, 1423-1432.	5.0	12
68	Quantitative proteomic approaches in biomarker discovery of inflammatory bowel disease. <i>Journal of Digestive Diseases</i> , 2012, 13, 497-503.	0.7	11
69	The efficacy of human placenta-derived mesenchymal stem cells on radiation enteropathy along with proteomic biomarkers predicting a favorable response. <i>Stem Cell Research and Therapy</i> , 2017, 8, 105.	2.4	11
70	De novo transcriptome profile of coccolithophorid alga <i>Emiliania huxleyi</i> CCMP371 at different calcium concentrations with proteome analysis. <i>PLoS ONE</i> , 2019, 14, e0221938.	1.1	11
71	Comparative Primary Metabolic and Lipidomic Profiling of Freshwater and Marine <i>Synechocystis</i> Strains Using by GC-MS and NanoESI-MS Analyses. <i>Biotechnology and Bioprocess Engineering</i> , 2020, 25, 308-319.	1.4	11
72	Effects of the timing of a culture temperature reduction on the comprehensive metabolite profiles of <i>Chlorella vulgaris</i> . <i>Journal of Applied Phycology</i> , 2016, 28, 2641-2650.	1.5	10

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73	TEMPO-Assisted Free Radical-Initiated Peptide Sequencing Mass Spectrometry (FRIPS MS) in Q-TOF and Orbitrap Mass Spectrometers: Single-Step Peptide Backbone Dissociations in Positive Ion Mode. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 154-163.	1.2	10
74	Development of an automated high-throughput sample preparation protocol for LC-MS/MS analysis of glycosylated peptides. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018, 1092, 88-94.	1.2	10
75	Enrichment and analysis of glycosylated proteins. <i>Reviews in Analytical Chemistry</i> , 2022, 41, 83-97.	1.5	10
76	Comparative Lipidomic Profiling of Two <i>Dunaliella tertiolecta</i> Strains with Different Growth Temperatures under Nitrate-Deficient Conditions. <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 880-887.	2.4	9
77	Phycobiliproteins Production Enhancement and Lipidomic Alteration by Titanium Dioxide Nanoparticles in <i>Synechocystis</i> sp. PCC 6803 Culture. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 8522-8529.	2.4	9
78	Label-free quantitative proteomic analysis of human periodontal ligament stem cells by high-resolution mass spectrometry. <i>Journal of Periodontal Research</i> , 2019, 54, 53-62.	1.4	9
79	Enhancement of the Antitumor Effect of Methotrexate on Colorectal Cancer Cells via Lactate Calcium Salt Targeting Methionine Metabolism. <i>Nutrition and Cancer</i> , 2017, 69, 663-673.	0.9	8
80	An automated high-throughput sample preparation method using double-filtration for serum metabolite LC-MS analysis. <i>Analytical Methods</i> , 2019, 11, 4060-4065.	1.3	8
81	Enhanced Production of Fatty Acids via Redirection of Carbon Flux in Marine Microalga <i>Tetraselmis</i> sp.. <i>Journal of Microbiology and Biotechnology</i> , 2018, 28, 267-274.	0.9	8
82	Different Regulatory Modes of <i>Synechocystis</i> sp. PCC 6803 in Response to Photosynthesis Inhibitory Conditions. <i>MSystems</i> , 2021, 6, e0094321.	1.7	7
83	Dietary walnut as food factor to rescue from NSAID-induced gastrointestinal mucosal damages. <i>Archives of Biochemistry and Biophysics</i> , 2020, 689, 108466.	1.4	6
84	Multi-Omic Analyses Reveal Habitat Adaptation of Marine Cyanobacterium <i>Synechocystis</i> sp. PCC 7338. <i>Frontiers in Microbiology</i> , 2021, 12, 667450.	1.5	6
85	Proteomic analysis of <i>Synechocystis</i> sp. PCC6803 responses to low-temperature and high light conditions. <i>Biotechnology and Bioprocess Engineering</i> , 2014, 19, 629-640.	1.4	5
86	Proteomic Profiling of <i>Emiliania huxleyi</i> Using a Three-Dimensional Separation Method Combined with Tandem Mass Spectrometry. <i>Molecules</i> , 2020, 25, 3028.	1.7	5
87	Proteomic Analysis of the Vitreous Body in Proliferative and Non-Proliferative Diabetic Retinopathy. <i>Current Proteomics</i> , 2021, 18, 143-152.	0.1	5
88	Proteomic and Metabolomic Analyses of Maggots in Porcine Corpses for Post-Mortem Interval Estimation. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 7885.	1.3	5
89	An Automated High Throughput Proteolysis and Desalting Platform for Quantitative Proteomic Analysis. <i>Mass Spectrometry Letters</i> , 2013, 4, 25-29.	0.5	5
90	A review of suspension trapping digestion method in bottom-up proteomics. <i>Journal of Separation Science</i> , 0, , .	1.3	5

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91	Comparative Proteomic Profiling of Marine and Freshwater Synechocystis Strains Using Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Marine Science and Engineering</i> , 2020, 8, 790.	1.2	4
92	Enhanced Production of Photosynthetic Pigments and Various Metabolites and Lipids in the Cyanobacteria <i>Synechocystis</i> sp. PCC 7338 Culture in the Presence of Exogenous Glucose. <i>Biomolecules</i> , 2021, 11, 214.	1.8	4
93	Photosynthetic production of biodiesel in <i>Synechocystis</i> sp. PCC6803 transformed with insect or plant fatty acid methyltransferase. <i>Bioprocess and Biosystems Engineering</i> , 2021, 44, 1433-1439.	1.7	4
94	Determining the Particle Size Distributions of Titanium Dioxide Using Sedimentation Field-Flow Fractionation and Photon Correlation Spectroscopy. <i>ACS Symposium Series</i> , 2001, , 285-298.	0.5	3
95	Regulation of IL-24 in human oral keratinocytes stimulated with <i>Tannerella forsythia</i> . <i>Molecular Oral Microbiology</i> , 2019, 34, 209-218.	1.3	3
96	Combined phospho- and glycoproteome enrichment in nephrocalcinosis tissues of phytate-fed rats. <i>Rapid Communications in Mass Spectrometry</i> , 2013, 27, 2767-2776.	0.7	2
97	An Automated High-Throughput Sample Preparation Protocol for LC-MS/MS Analysis of Glycopeptides. <i>Current Proteomics</i> , 2016, 13, 55-60.	0.1	2
98	Discovery of Post-Translational Modifications in <i>Emiliana huxleyi</i> . <i>Molecules</i> , 2021, 26, 2027.	1.7	2
99	Use of Filter-Aided Capture and Elution Protocol for Concurrent Preparation of N-glycan and O-glycopeptides for LC-MS/MS Analysis. <i>Current Proteomics</i> , 2016, 13, 48-54.	0.1	1
100	Liquid Chromatography/Electrospray Ionization Tandem Mass Spectrometry-based Structural Analysis of Deacylated Lipooligosaccharides From <i>Escherichia coli</i> . <i>Bulletin of the Korean Chemical Society</i> , 2020, 41, 454-459.	1.0	1
101	A Quantitative Proteomic Analysis to Reveal Effects of N-acetylcysteine on H ₂ O ₂ -induced Cytotoxicity. <i>Current Proteomics</i> , 2021, 18, 403-414.	0.1	1
102	Use of High-Throughput Trypsin Digestion in Proteomic Studies. <i>Current Proteomics</i> , 2016, 12, 210-216.	0.1	1
103	ldBean: a Java GUI application for conversion of biological identifiers. <i>BMB Reports</i> , 2011, 44, 107-112.	1.1	1
104	Effects of Heat Shock Treatment on Enzymatic Proteolysis for LC-MS/MS Quantitative Proteome Analysis. <i>Mass Spectrometry Letters</i> , 2016, 7, 1-11.	0.5	1
105	Advances of LC-MS and CZE-MS in proteome analysis. , 2006, , .		0
106	Human Plasma PeptideAtlas. , 0, , 317-322.		0
107	Proteome Analysis of Mouse Adipose Tissue and Colon Tissue using a Novel Integrated Data Processing Pipeline. <i>Mass Spectrometry Letters</i> , 2014, 5, 16-23.	0.5	0