

Hookeun Lee

List of Publications by Year in descending order

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107
papers

5,057
citations

94269

37
h-index

91712

69
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107
all docs

107
docs citations

107
times ranked

6512
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Enrichment and analysis of glycosylated proteins. <i>Reviews in Analytical Chemistry</i> , 2022, 41, 83-97.	1.5	10
3	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
4	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
5	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
6	Establishment of functional epithelial organoids from human lacrimal glands. <i>Stem Cell Research and Therapy</i> , 2021, 12, 247.	2.4	18
7	Discovery of Post-Translational Modifications in <i>Emiliana huxleyi</i> . <i>Molecules</i> , 2021, 26, 2027.	1.7	2
8	Proteomics in Forensic Analysis: Applications for Human Samples. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 3393.	1.3	21
9	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
10	Proteomic Analysis of the Vitreous Body in Proliferative and Non-Proliferative Diabetic Retinopathy. <i>Current Proteomics</i> , 2021, 18, 143-152.	0.1	5
11	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
12	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
13	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
14	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
15	Current Status and Future Strategies to Increase Secondary Metabolite Production from Cyanobacteria. <i>Microorganisms</i> , 2020, 8, 1849.	1.6	21
16	Comparative Proteomic Profiling of Marine and Freshwater <i>Synechocystis</i> Strains Using Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Marine Science and Engineering</i> , 2020, 8, 790.	1.2	4
17	Comparative Primary Metabolic and Lipidomic Profiling of Freshwater and Marine <i>Synechocystis</i> Strains Using GC-MS and NanoESI-MS Analyses. <i>Biotechnology and Bioprocess Engineering</i> , 2020, 25, 308-319.	1.4	11
18	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

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19	Dietary walnut as food factor to rescue from NSAID-induced gastrointestinal mucosal damages. Archives of Biochemistry and Biophysics, 2020, 689, 108466.	1.4	6
20	Proteomic Profiling of <i>Emiliania huxleyi</i> Using a Three-Dimensional Separation Method Combined with Tandem Mass Spectrometry. Molecules, 2020, 25, 3028.	1.7	5
21	Review of Three-Dimensional Liquid Chromatography Platforms for Bottom-Up Proteomics. International Journal of Molecular Sciences, 2020, 21, 1524.	1.8	50
22	Discovery of plasma biomarkers for predicting the severity of coronary artery atherosclerosis by quantitative proteomics. BMJ Open Diabetes Research and Care, 2020, 8, e001152.	1.2	19
23	Regulation of IL-24 in human oral keratinocytes stimulated with <i>Tannerella forsythia</i> . Molecular Oral Microbiology, 2019, 34, 209-218.	1.3	3
24	An automated high-throughput sample preparation method using double-filtration for serum metabolite LC-MS analysis. Analytical Methods, 2019, 11, 4060-4065.	1.3	8
25	De novo transcriptome profile of coccolithophorid alga <i>Emiliania huxleyi</i> CCMP371 at different calcium concentrations with proteome analysis. PLoS ONE, 2019, 14, e0221938.	1.1	11
26	Proteogenomic Characterization of Human Early-Onset Gastric Cancer. Cancer Cell, 2019, 35, 111-124.e10.	7.7	183
27	Neural Ganglia Transcriptome and Peptidome Associated with Sexual Maturation in Female Pacific Abalone (<i>Haliotis discus hannai</i>). Genes, 2019, 10, 268.	1.0	18
28	Label-free quantitative proteomic analysis of human periodontal ligament stem cells by high-resolution mass spectrometry. Journal of Periodontal Research, 2019, 54, 53-62.	1.4	9
29	Phycobiliproteins Production Enhancement and Lipidomic Alteration by Titanium Dioxide Nanoparticles in <i>Synechocystis</i> sp. PCC 6803 Culture. Journal of Agricultural and Food Chemistry, 2018, 66, 8522-8529.	2.4	9
30	Effects of FGF-21-secreting adipose-derived stem cells in thioacetamide-induced hepatic fibrosis. Journal of Cellular and Molecular Medicine, 2018, 22, 5165-5169.	1.6	19
31	Development of an automated high-throughput sample preparation protocol for LC-MS/MS analysis of glycosylated peptides. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2018, 1092, 88-94.	1.2	10
32	Enhanced Production of Fatty Acids via Redirection of Carbon Flux in Marine Microalga <i>Tetraselmis</i> sp.. Journal of Microbiology and Biotechnology, 2018, 28, 267-274.	0.9	8
33	The efficacy of human placenta-derived mesenchymal stem cells on radiation enteropathy along with proteomic biomarkers predicting a favorable response. Stem Cell Research and Therapy, 2017, 8, 105.	2.4	11
34	Enhancement of the Antitumor Effect of Methotrexate on Colorectal Cancer Cells via Lactate Calcium Salt Targeting Methionine Metabolism. Nutrition and Cancer, 2017, 69, 663-673.	0.9	8
35	Enhanced production of fatty acids in three strains of microalgae using a combination of nitrogen starvation and chemical inhibitors of carbohydrate synthesis. Biotechnology and Bioprocess Engineering, 2017, 22, 60-67.	1.4	14
36	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. Journal of the American Society for Mass Spectrometry, 2017, 28, 154-163.	1.2	10

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37	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
38	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
39	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
40	Genome-wide transcriptome analysis revealed organelle specific responses to temperature variations in algae. <i>Scientific Reports</i> , 2016, 6, 37770.	1.6	38
41	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
42	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
43	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
44	Use of High-Throughput Trypsin Digestion in Proteomic Studies. <i>Current Proteomics</i> , 2016, 12, 210-216.	0.1	1
45	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
46	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
47	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
48	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
49	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
50	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
51	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
52	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
53	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
54	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

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55	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
56	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
57	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
58	An Automated High Throughput Proteolysis and Desalting Platform for Quantitative Proteomic Analysis. <i>Mass Spectrometry Letters</i> , 2013, 4, 25-29.	0.5	5
59	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
60	Quantitative proteomic approaches in biomarker discovery of inflammatory bowel disease. <i>Journal of Digestive Diseases</i> , 2012, 13, 497-503.	0.7	11
61	Ultrasmall gold nanoparticles for highly specific isolation/enrichment of N-linked glycosylated peptides. <i>Analyst</i> , 2012, 137, 991-998.	1.7	28
62	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
63	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> , 2011, 136, 2100.	1.7	14
64	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
65	IdBean: a Java GUI application for conversion of biological identifiers. <i>BMB Reports</i> , 2011, 44, 107-112.	1.1	1
66	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
67	Combining selected reaction monitoring with discovery proteomics in limited biological samples. <i>Proteomics</i> , 2009, 9, 4834-4836.	1.3	17
68	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
69	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
70	Quantitative Proteomic Analysis of Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 326-346.	2.5	99
71	MS-BID: a Java package for label-free LC-MS-based comparative proteomic analysis. <i>Bioinformatics</i> , 2008, 24, 2641-2642.	1.8	12
72	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

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73	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
74	Computational prediction of proteotypic peptides for quantitative proteomics. <i>Nature Biotechnology</i> , 2007, 25, 125-131.	9.4	653
75	A high-quality catalog of the <i>Drosophila melanogaster</i> proteome. <i>Nature Biotechnology</i> , 2007, 25, 576-583.	9.4	247
76	Advances in proteomic workflows for systems biology. <i>Current Opinion in Biotechnology</i> , 2007, 18, 378-384.	3.3	95
77	Analysis of the <i>Saccharomyces cerevisiae</i> proteome with PeptideAtlas. <i>Genome Biology</i> , 2006, 7, R106.	13.9	60
78	UniPep—a database for human N-linked glycosites: a resource for biomarker discovery. <i>Genome Biology</i> , 2006, 7, R73.	13.9	101
79	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
80	Advances of LC-MS and CZE-MS in proteome analysis. , 2006, , .		0
81	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
82	Signal Maps for Mass Spectrometry-based Comparative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 423-432.	2.5	110
83	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
84	Quantitative Proteomic Analysis of Myc-induced Apoptosis. <i>Journal of Biological Chemistry</i> , 2006, 281, 2750-2756.	1.6	65
85	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
86	Human Plasma PeptideAtlas. <i>Proteomics</i> , 2005, 5, 3497-3500.	1.3	132
87	Proteomic Identification of Potential Susceptibility Factors in Drug-Induced Liver Disease. <i>Chemical Research in Toxicology</i> , 2005, 18, 924-933.	1.7	75
88	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
89	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
90	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

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91	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
92	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
93	Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry. <i>Genome Biology</i> , 2004, 6, R9.	13.9	252
94	System-based proteomic analysis of the interferon response in human liver cells. <i>Genome Biology</i> , 2004, 5, R54.	13.9	63
95	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
96	Abundance Ratio-Dependent Proteomic Analysis by Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 867-874.	3.2	62
97	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
98	Development of a Multiplexed Microcapillary Liquid Chromatography System for High-Throughput Proteome Analysis. <i>Analytical Chemistry</i> , 2002, 74, 4353-4360.	3.2	55
99	Approaching complete peroxisome characterization by gas-phase fractionation. <i>Electrophoresis</i> , 2002, 23, 3205-3216.	1.3	193
100	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
101	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
102	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
103	Evaluation of Different Field-Flow Fractionation Techniques for Separating Bacteria. <i>Separation Science and Technology</i> , 2000, 35, 1761-1775.	1.3	35
104	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
105	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
106	Human Plasma PeptideAtlas. , 0, , 317-322.		0
107	A review of suspension trapping digestion method in bottom-up proteomics. <i>Journal of Separation Science</i> , 0, , .	1.3	5