

Hookeun Lee

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

101
papers

4,236
citations

33
h-index

64
g-index

107
ext. papers

4,675
ext. citations

6.3
avg, IF

4.78
L-index

#	Paper	IF	Citations
101	Enrichment and analysis of glycated proteins. <i>Reviews in Analytical Chemistry</i> , 2022 , 41, 83-97	2.3	1
100	Establishment of functional epithelial organoids from human lacrimal glands. <i>Stem Cell Research and Therapy</i> , 2021 , 12, 247	8.3	3
99	Proteomics in Forensic Analysis: Applications for Human Samples. <i>Applied Sciences (Switzerland)</i> , 2021 , 11, 3393	2.6	3
98	Multi-Omic Analyses Reveal Habitat Adaptation of Marine Cyanobacterium sp. PCC 7338. <i>Frontiers in Microbiology</i> , 2021 , 12, 667450	5.7	2
97	Proteomic Analysis of the Vitreous Body in Proliferative and Non-Proliferative Diabetic Retinopathy. <i>Current Proteomics</i> , 2021 , 18, 143-152	0.7	3
96	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	3.2	6
95	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	3.7	1
94	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	0.7	1
93	Proteomic and Metabolomic Analyses of Maggots in Porcine Corpses for Post-Mortem Interval Estimation. <i>Applied Sciences (Switzerland)</i> , 2021 , 11, 7885	2.6	
92	Different Regulatory Modes of sp. PCC 6803 in Response to Photosynthesis Inhibitory Conditions. <i>MSystems</i> , 2021 , e0094321	7.6	0
91	Current Status and Future Strategies to Increase Secondary Metabolite Production from Cyanobacteria. <i>Microorganisms</i> , 2020 , 8,	4.9	9
90	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	2.4	2
89	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	3.1	6
88	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	1.2	1
87	Dietary walnut as food factor to rescue from NSAID-induced gastrointestinal mucosal damages. <i>Archives of Biochemistry and Biophysics</i> , 2020 , 689, 108466	4.1	2
86	Proteomic Profiling of Using a Three-Dimensional Separation Method Combined with Tandem Mass Spectrometry. <i>Molecules</i> , 2020 , 25,	4.8	3
85	Review of Three-Dimensional Liquid Chromatography Platforms for Bottom-Up Proteomics. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	31

84	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,	4.5	7
83	UBA2 activates Wnt/βcatenin 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	8.3	6
82	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	3.7	7
81	Proteogenomic Characterization of Human Early-Onset Gastric Cancer. <i>Cancer Cell</i> , 2019 , 35, 111-124.e104.3	10.3	95
80	Neural Ganglia Transcriptome and Peptidome Associated with Sexual Maturation in Female Pacific Abalone (<i>Haliotis</i>). <i>Genes</i> , 2019 , 10,	4.2	11
79	Regulation of IL-24 in human oral keratinocytes stimulated with <i>Tannerella forsythia</i> . <i>Molecular Oral Microbiology</i> , 2019 , 34, 209-218	4.6	0
78	An automated high-throughput sample preparation method using double-filtration for serum metabolite LC-MS analysis. <i>Analytical Methods</i> , 2019 , 11, 4060-4065	3.2	6
77	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	4.3	5
76	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	5.7	6
75	Effects of FGF21-secreting adipose-derived stem cells in thioacetamide-induced hepatic fibrosis. <i>Journal of Cellular and Molecular Medicine</i> , 2018 , 22, 5165-5169	5.6	11
74	Development of an automated high-throughput sample preparation protocol for LC-MS/MS analysis of glycated peptides. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018 , 1092, 88-94	3.2	8
73	Enhanced Production of Fatty Acids via Redirection of Carbon Flux in Marine Microalga sp. <i>Journal of Microbiology and Biotechnology</i> , 2018 , 28, 267-274	3.3	5
72	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	8.3	8
71	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	2.8	6
70	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	3.1	10
69	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	3.5	7
68	Genome-wide transcriptome analysis revealed organelle specific responses to temperature variations in algae. <i>Scientific Reports</i> , 2016 , 6, 37770	4.9	28
67	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	5.1	12

66	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	3.2	4
65	Efficient protein digestion using highly-stable and reproducible trypsin coatings on magnetic nanofibers. <i>Chemical Engineering Journal</i> , 2016 , 288, 770-777	14.7	14
64	Effects of Heat Shock Treatment on Enzymatic Proteolysis for LC-MS/MS Quantitative Proteome Analysis. <i>Mass Spectrometry Letters</i> , 2016 , 7, 1-11		1
63	An Automated High-Throughput Sample Preparation Protocol for LC-MS/MS Analysis of Glycopeptides. <i>Current Proteomics</i> , 2016 , 13, 55-60	0.7	2
62	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	0.7	1
61	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, 4807-16	5.7	27
60	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	11	32
59	Integrated analysis of global proteome, phosphoproteome, and glycoproteome enables complementary interpretation of disease-related protein networks. <i>Scientific Reports</i> , 2015 , 5, 18189	4.9	23
58	Development of an Automated, High-throughput Sample Preparation Protocol for Proteomics Analysis. <i>Bulletin of the Korean Chemical Society</i> , 2015 , 36, 1791-1798	1.2	10
57	Proteomic analysis of serum from patients with major depressive disorder to compare their depressive and remission statuses. <i>Psychiatry Investigation</i> , 2015 , 12, 249-59	3.1	33
56	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, 880-7	5.7	6
55	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	3.9	15
54	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	4.8	33
53	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	3.1	2
52	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		
51	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, 166-74	3.3	29
50	Combined phospho- and glycoproteome enrichment in nephrocalcinosis tissues of phytate-fed rats. <i>Rapid Communications in Mass Spectrometry</i> , 2013 , 27, 2767-76	2.2	2
49	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	3.7	44

48	An Automated High Throughput Proteolysis and Desalting Platform for Quantitative Proteomic Analysis. <i>Mass Spectrometry Letters</i> , 2013 , 4, 25-29		5
47	Quantitative proteomic approaches in biomarker discovery of inflammatory bowel disease. <i>Journal of Digestive Diseases</i> , 2012 , 13, 497-503	3.3	10
46	Ultrasmall gold nanoparticles for highly specific isolation/enrichment of N-linked glycosylated peptides. <i>Analyst, The</i> , 2012 , 137, 991-8	5	28
45	Protein expression changes in ovarian cancer during the transition from benign to malignant. <i>Journal of Proteome Research</i> , 2012 , 11, 2876-89	5.6	36
44	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	3.9	27
43	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, 20267-76	16.4	81
42	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, The</i> , 2011 , 136, 2100-5	5	12
41	IdBean: a Java GUI application for conversion of biological identifiers. <i>BMB Reports</i> , 2011 , 44, 107-12	5.5	1
40	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, 8510-8	7.8	16
39	Combining selected reaction monitoring with discovery proteomics in limited biological samples. <i>Proteomics</i> , 2009 , 9, 4834-6	4.8	13
38	Proteome analysis of Legionella vacuoles purified by magnetic immunoseparation reveals secretory and endosomal GTPases. <i>Traffic</i> , 2009 , 10, 76-87	5.7	129
37	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	5.6	134
36	Quantitative proteomic analysis of protein complexes: concurrent identification of interactors and their state of phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 326-46	7.6	95
35	MS-BID: a Java package for label-free LC-MS-based comparative proteomic analysis. <i>Bioinformatics</i> , 2008 , 24, 2641-2	7.2	9
34	Computational prediction of proteotypic peptides for quantitative proteomics. <i>Nature Biotechnology</i> , 2007 , 25, 125-31	44.5	582
33	A high-quality catalog of the Drosophila melanogaster proteome. <i>Nature Biotechnology</i> , 2007 , 25, 576-83	44.5	230
32	Advances in proteomic workflows for systems biology. <i>Current Opinion in Biotechnology</i> , 2007 , 18, 378-84	11.4	86
31	Assessing bias in experiment design for large scale mass spectrometry-based quantitative proteomics. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1741-8	7.6	44

30	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	3.1	35
29	Signal maps for mass spectrometry-based comparative proteomics. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 423-32	7.6	96
28	Proteome analysis of Halobacterium sp. NRC-1 facilitated by the biomodule analysis tool BMSorter. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 987-97	7.6	13
27	Quantitative proteomic analysis of myc-induced apoptosis: a direct role for Myc induction of the mitochondrial chloride ion channel, mtCLIC/CLIC4. <i>Journal of Biological Chemistry</i> , 2006 , 281, 2750-6	5.4	63
26	Analysis of the Saccharomyces cerevisiae proteome with PeptideAtlas. <i>Genome Biology</i> , 2006 , 7, R106	18.3	51
25	UniPep--a database for human N-linked glycosites: a resource for biomarker discovery. <i>Genome Biology</i> , 2006 , 7, R73	18.3	94
24	Optimized peptide separation and identification for mass spectrometry based proteomics via free-flow electrophoresis. <i>Journal of Proteome Research</i> , 2006 , 5, 2241-9	5.6	78
23	Quantitative proteomic analysis of the budding yeast cell cycle using acid-cleavable isotope-coded affinity tag reagents. <i>Proteomics</i> , 2006 , 6, 6146-57	4.8	33
22	Proteomic identification of potential susceptibility factors in drug-induced liver disease. <i>Chemical Research in Toxicology</i> , 2005 , 18, 924-33	4	67
21	Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry. <i>Genome Biology</i> , 2005 , 6, R9	18.3	233
20	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, 380-7	4.8	105
19	Human Plasma PeptideAtlas. <i>Proteomics</i> , 2005 , 5, 3497-500	4.8	121
18	Quantitative proteomic analysis of metabolic regulation by copper ions in Methylococcus capsulatus (Bath). <i>Journal of Biological Chemistry</i> , 2004 , 279, 51554-60	5.4	71
17	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, 1039-41	7.6	49
16	Gene expression analyzed by high-resolution state array analysis and quantitative proteomics: response of yeast to mating pheromone. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 478-89	7.6	158
15	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, 101-10	3.2	27
14	A tool to visualize and evaluate data obtained by liquid chromatography-electrospray ionization-mass spectrometry. <i>Analytical Chemistry</i> , 2004 , 76, 3856-60	7.8	83
13	System-based proteomic analysis of the interferon response in human liver cells. <i>Genome Biology</i> , 2004 , 5, R54	18.3	55

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, 2093-8	2.2	96
11	Abundance ratio-dependent proteomic analysis by mass spectrometry. <i>Analytical Chemistry</i> , 2003 , 75, 867-74	7.8	55
10	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, 2746-52	7.8	70
9	Approaching complete peroxisome characterization by gas-phase fractionation. <i>Electrophoresis</i> , 2002 , 23, 3205-16	3.6	173
8	Development of a multiplexed microcapillary liquid chromatography system for high-throughput proteome analysis. <i>Analytical Chemistry</i> , 2002 , 74, 4353-60	7.8	54
7	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, 1238-46	3.5	80
6	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	0.4	3
5	Analysis of self-assembled cationic lipid-DNA gene carrier complexes using flow field-flow fractionation and light scattering. <i>Analytical Chemistry</i> , 2001 , 73, 837-43	7.8	66
4	Evaluation of Different Field-Flow Fractionation Techniques for Separating Bacteria. <i>Separation Science and Technology</i> , 2000 , 35, 1761-1775	2.5	30
3	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	2.8	14
2	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, 2495-503	7.8	26
1	Human Plasma PeptideAtlas317-322		