

Kun Cho

List of Publications by Year in descending order

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62
papers

1,541
citations

331670

21
h-index

330143

37
g-index

62
all docs

62
docs citations

62
times ranked

2650
citing authors

#	ARTICLE	IF	CITATIONS
1	Label-free proteomics approach reveals candidate proteins in rice (<i>Oryza sativa</i> L.) important for ACC deaminase producing bacteria-mediated tolerance against salt stress. <i>Environmental Microbiology</i> , 2022, 24, 3612-3624.	3.8	21
2	Shotgun proteomics of extracellular matrix in late senescent human dermal fibroblasts reveals a down-regulated fibronectin-centered network. <i>Journal of Analytical Science and Technology</i> , 2022, 13, .	2.1	2
3	Analysis of hair and plasma samples for methotrexate (MTX) and metabolite using high-performance liquid chromatography triple quadrupole mass spectrometry (LC-MS/MS) detection. <i>Journal of Mass Spectrometry</i> , 2021, 56, e4648.	1.6	7
4	Proteome Changes Reveal the Protective Roles of Exogenous Citric Acid in Alleviating Cu Toxicity in <i>Brassica napus</i> L.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5879.	4.1	9
5	Label-free quantitative proteomic analysis of serum extracellular vesicles differentiating patients of alcoholic and nonalcoholic fatty liver diseases. <i>Journal of Proteomics</i> , 2021, 245, 104278.	2.4	10
6	Compositional Characteristics of Glucuronide Conjugates in Regional <i>Glechoma hederacea</i> var. <i>longituba</i> Herbal Extracts Using a Set of Polyphenolic Marker Compounds. <i>Plants</i> , 2021, 10, 2353.	3.5	2
7	Identification of Polyphenol Glucuronide Conjugates in <i>Glechoma hederacea</i> var. <i>longituba</i> Hot Water Extracts by High-Performance Liquid Chromatography-Tandem Mass Spectrometry (HPLC-MS/MS). <i>Molecules</i> , 2020, 25, 4713.	3.8	7
8	Selective Identification of β -Galactosyl Epitopes in N-Glycoproteins Using Characteristic Fragment Ions from Higher-Energy Collisional Dissociation. <i>Analytical Chemistry</i> , 2020, 92, 13144-13154.	6.5	6
9	Comparative Proteomic Analysis in Scar-Free Skin Regeneration in <i>Acomys cahirinus</i> and Scarring <i>Mus musculus</i> . <i>Scientific Reports</i> , 2020, 10, 166.	3.3	15
10	Recent developments in pre-treatment and analytical techniques for synthetic polymers by MALDI-TOF mass spectrometry. <i>Analytical Methods</i> , 2020, 12, 5767-5800.	2.7	12
11	Molecular profiling of a γ -type high molecular weight glutenin subunit at Glu-D1 locus from a North Korean landrace wheat (<i>Triticum aestivum</i> L.). <i>Plant Biotechnology Reports</i> , 2018, 12, 139-148.	1.5	2
12	Evidence of link between quorum sensing and sugar metabolism in <i>Escherichia coli</i> revealed via cocystal structures of LsrK and HPr. <i>Science Advances</i> , 2018, 4, eaar7063.	10.3	68
13	Overexpression of the Bx7 high molecular weight glutenin subunit on the Glu-B1 locus in a Korean wheat landrace. <i>Plant Biotechnology Reports</i> , 2017, 11, 97-105.	1.5	12
14	Characterization of a novel γ -type high molecular weight glutenin subunit at Glu-D1 locus. <i>Genes and Genomics</i> , 2017, 39, 957-965.	1.4	1
15	Pyrazole derived ultra-short antimicrobial peptidomimetics with potent anti-biofilm activity. <i>European Journal of Medicinal Chemistry</i> , 2017, 125, 551-564.	5.5	60
16	Human salivary proteins with affinity to lipoteichoic acid of <i>Enterococcus faecalis</i> . <i>Molecular Immunology</i> , 2016, 77, 52-59.	2.2	7
17	Differential profiles of gastrointestinal proteins interacting with peptidoglycans from <i>Lactobacillus plantarum</i> and <i>Staphylococcus aureus</i> . <i>Molecular Immunology</i> , 2015, 65, 77-85.	2.2	23
18	Protein profiles in mucosal and systemic compartments in response to <i>Vibrio cholerae</i> in a mouse pulmonary infection model. <i>Microbial Pathogenesis</i> , 2015, 86, 10-17.	2.9	0

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19	Protein Profiling Reveals Novel Proteins in Pollen and Pistil of W22 (ga1; Ga1) in Maize. <i>Proteomes</i> , 2014, 2, 258-271.	3.5	4
20	Proteome analysis of roots of wheat seedlings under aluminum stress. <i>Molecular Biology Reports</i> , 2014, 41, 671-681.	2.3	43
21	Phosphorylation of Hepatitis C Virus RNA Polymerases Ser29 and Ser42 by Protein Kinase C-Related Kinase 2 Regulates Viral RNA Replication. <i>Journal of Virology</i> , 2014, 88, 11240-11252.	3.4	20
22	Profiling of mitochondrial proteome in wheat roots. <i>Molecular Biology Reports</i> , 2014, 41, 5359-5366.	2.3	8
23	Proteomic analysis of the effect of retinoic acids on the human breast cancer cell line MCF-7. <i>Molecular Biology Reports</i> , 2014, 41, 3499-3507.	2.3	8
24	Characterization of N-linked Glycan Structures Using Normal-phase Capillary LC-MALDI Tandem Mass Spectrometry. <i>Bulletin of the Korean Chemical Society</i> , 2014, 35, 955-957.	1.9	0
25	Patterns of protein expression in water-stressed wheat chloroplasts. <i>Biologia Plantarum</i> , 2013, 57, 305-312.	1.9	26
26	Investigation of adipocyte proteome during the differentiation of brown preadipocytes. <i>Journal of Proteomics</i> , 2013, 94, 327-336.	2.4	20
27	The wheat chloroplastic proteome. <i>Journal of Proteomics</i> , 2013, 93, 326-342.	2.4	33
28	Profiling and semiquantitative analysis of the cell surface proteome in human mesenchymal stem cells. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 5501-5517.	3.7	5
29	Hrp3 controls nucleosome positioning to suppress non-coding transcription in eu- and heterochromatin. <i>EMBO Journal</i> , 2012, 31, 4375-4387.	7.8	55
30	Osmotic Stress Regulates Mammalian Target of Rapamycin (mTOR) Complex 1 via c-Jun N-terminal Kinase (JNK)-mediated Raptor Protein Phosphorylation. <i>Journal of Biological Chemistry</i> , 2012, 287, 18398-18407.	3.4	37
31	Chemical Interaction of Alexidine and Sodium Hypochlorite. <i>Journal of Endodontics</i> , 2012, 38, 112-116.	3.1	24
32	Comparative proteomic analysis of early salt stress-responsive proteins in roots of SnRK2 transgenic rice. <i>Proteome Science</i> , 2012, 10, 25.	1.7	89
33	Towards an understanding of wheat chloroplasts: a methodical investigation of thylakoid proteome. <i>Molecular Biology Reports</i> , 2012, 39, 5069-5083.	2.3	24
34	Changes in physiology and protein abundance in salt-stressed wheat chloroplasts. <i>Molecular Biology Reports</i> , 2012, 39, 9059-9074.	2.3	93
35	Protein Analysis Using a Combination of an Online Monolithic Trypsin Immobilized Enzyme Reactor and Collisionally-Activated Dissociation/Electron Transfer Dissociation Dual Tandem Mass Spectrometry. <i>Bulletin of the Korean Chemical Society</i> , 2012, 33, 3233-3240.	1.9	3
36	A Multidimensional System for Phosphopeptide Analysis Using TiO ₂ Enrichment and Ion-exchange Chromatography with Mass Spectrometry. <i>Bulletin of the Korean Chemical Society</i> , 2012, 33, 3298-3302.	1.9	3

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37	Quantitative Phosphoproteomics of the Human Neural Stem Cell Differentiation into Oligodendrocyte by Mass Spectrometry. <i>Mass Spectrometry Letters</i> , 2012, 3, 93-100.	0.5	3
38	Comparative secretome analysis of human follicular dermal papilla cells and fibroblasts using shotgun proteomics. <i>BMB Reports</i> , 2012, 45, 253-258.	2.4	33
39	Identification of <i>Porphyromonas gingivalis</i> lipopolysaccharide-binding proteins in human saliva. <i>Molecular Immunology</i> , 2011, 48, 2207-2213.	2.2	44
40	Quantitative Proteomic Analysis of Cell Wall and Plasma Membrane Fractions from Multidrug-Resistant <i>Acinetobacter baumannii</i> . <i>Journal of Proteome Research</i> , 2011, 10, 459-469.	3.7	57
41	High Accuracy Mass Measurement Approach in the Identification of Phospholipids in Lipid Extracts: 7 T Fourier-transform Mass Spectrometry and MS/MS Validation. <i>Bulletin of the Korean Chemical Society</i> , 2011, 32, 1170-1178.	1.9	1
42	Systematic cyanobacterial membrane proteome analysis by combining acid hydrolysis and digestive enzymes with nano-liquid chromatography- ¹³ C Fourier transform mass spectrometry. <i>Journal of Chromatography A</i> , 2010, 1217, 285-293.	3.7	27
43	Sequential Fe ₃ O ₄ /TiO ₂ enrichment for phosphopeptide analysis by liquid chromatography/tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 1467-1474.	1.5	18
44	Differential Protein Quantitation in Mouse Neuronal Cell Lines using Amine-Reactive Isobaric Tagging Reagents with Tandem Mass Spectrometry. <i>Mass Spectrometry Letters</i> , 2010, 1, 25-28.	0.2	0
45	Reinterpretation of the protein identification process for proteomics data. <i>Interdisciplinary Bio Central</i> , 2009, 1, 9.1-9.6.	0.1	0
46	Differential expression of cell surface proteins in human bone marrow mesenchymal stem cells cultured with or without basic fibroblast growth factor containing medium. <i>Proteomics</i> , 2009, 9, 4389-4405.	2.2	29
47	Comparative proteome analysis using amine-reactive isobaric tagging reagents coupled with 2D LC/MS/MS in 3T3-L1 adipocytes following hypoxia or normoxia. <i>Biochemical and Biophysical Research Communications</i> , 2009, 383, 135-140.	2.1	17
48	Proteome analysis of greenhouse-cultured lettuce with the natural soil mineral conditioner illite. <i>Soil Biology and Biochemistry</i> , 2008, 40, 1370-1378.	8.8	7
49	Human Microglial Cells Synthesize Albumin in Brain. <i>PLoS ONE</i> , 2008, 3, e2829.	2.5	76
50	Human microglial cells synthesize albumin in brain. <i>Nature Precedings</i> , 2008, , .	0.1	1
51	Protein phosphorylation analysis by site-specific arginine-mimic labeling in gel electrophoresis and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Analytical Biochemistry</i> , 2007, 370, 77-86.	2.4	11
52	Arginine-mimic labeling with guanidinoethanethiol to increase mass sensitivity of lysine-terminated phosphopeptides by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 2204-2210.	1.5	14
53	Efficient enrichment and desalting of protein digests using magnetic mesocellular carbon foams in matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 3435-3442.	1.5	4
54	Coupling of TiO ₂ -mediated enrichment and on-bead guanidinoethanethiol labeling for effective phosphopeptide analysis by matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 3987-3994.	1.5	14

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55	Analysis of aromatic catabolic pathways in <i>Pseudomonas putida</i> KTâ€...2440 using a combined proteomic approach: 2-DE/MS and cleavable isotope-coded affinity tag analysis. <i>Proteomics</i> , 2006, 6, 1301-1318.	2.2	150
56	A rice dehydration-inducible SNF1-related protein kinase 2 phosphorylates an abscisic acid responsive element-binding factor and associates with ABA signaling. <i>Plant Molecular Biology</i> , 2006, 63, 151-169.	3.9	113
57	Utility of electrophoretically derived protein mass estimates as additional constraints in proteome analysis of human serum based on MS/MS analysis. <i>Proteomics</i> , 2005, 5, 3376-3385.	2.2	30
58	Dynamic identification of phosphopeptides using immobilized metal ion affinity chromatography enrichment, subsequent partial β -elimination/chemical tagging and matrix-assisted laser desorption/ionization mass spectrometric analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 2495-2501.	1.5	18
59	Proteome analysis of hairy root from <i>Panax ginseng</i> C. A. Meyer using peptide fingerprinting, internal sequencing and expressed sequence tag data. <i>Proteomics</i> , 2003, 3, 2379-2392.	2.2	63
60	Enhanced detection and characterization of protocatechuate 3,4-dioxygenase in <i>Acinetobacter lwoffii</i> K24 by proteomics using a column separation. <i>Biochemical and Biophysical Research Communications</i> , 2002, 295, 903-909.	2.1	34
61	Structural determination of hexadecanoic lysophosphatidylcholine regioisomers by fast atom bombardment tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2002, 16, 2089-2093.	1.5	9
62	Structural determination of lysophosphatidylcholines extracted from marine sponges by fast atom bombardment tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 1120-1126.	1.5	9