

# Kai Cheng

## 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.

83  
papers

3,291  
citations

31  
h-index

55  
g-index

89  
ext. papers

4,051  
ext. citations

8.3  
avg, IF

4.94  
L-index

#	Paper	IF	Citations
83	Exploring the Microbiome-Wide Lysine Acetylation, Succinylation, and Propionylation in Human Gut Microbiota. <i>Analytical Chemistry</i> , <b>2021</b> , 93, 6594-6598	7.8	2
82	Elevated colonic microbiota-associated paucimannosidic and truncated N-glycans in pediatric ulcerative colitis. <i>Journal of Proteomics</i> , <b>2021</b> , 249, 104369	3.9	2
81	A simultaneous identification and quantification strategy for determination of sulfhydryl-containing metabolites in normal- and high-fat diet hamsters using stable isotope labeling combined with LC-MS. <i>Analytica Chimica Acta</i> , <b>2021</b> , 1184, 339016	6.6	1
80	Histone tales: lysine methylation, a protagonist in Arabidopsis development. <i>Journal of Experimental Botany</i> , <b>2020</b> , 71, 793-807	7	14
79	MetaLab 2.0 Enables Accurate Post-Translational Modifications Profiling in Metaproteomics. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2020</b> , 31, 1473-1482	3.5	6
78	RapidAIM: a culture- and metaproteomics-based Rapid Assay of Individual Microbiome responses to drugs. <i>Microbiome</i> , <b>2020</b> , 8, 33	16.6	39
77	Differential Lysis Approach Enables Selective Extraction of Taxon-Specific Proteins for Gut Metaproteomics. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 5379-5386	7.8	3
76	Chemoenzymatic Method for Glycoproteomic N-Glycan Type Quantitation. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 1618-1627	7.8	3
75	Metaproteomics Reveals Growth Phase-Dependent Responses of an Gut Microbiota to Metformin. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2020</b> , 31, 1448-1458	3.5	3
74	An in vitro model maintaining taxon-specific functional activities of the gut microbiome. <i>Nature Communications</i> , <b>2019</b> , 10, 4146	17.4	30
73	Proteomics analysis of site-specific glycoforms by a virtual multistage mass spectrometry method. <i>Analytica Chimica Acta</i> , <b>2019</b> , 1070, 60-68	6.6	10
72	Pharmacokinetic properties of wogonin and its herb-drug interactions with docetaxel in rats with mammary tumors. <i>Biomedical Chromatography</i> , <b>2018</b> , 32, e4264	1.7	6
71	Dual T and T weighted magnetic resonance imaging based on Gd loaded bioinspired melanin dots. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , <b>2018</b> , 14, 1743-1752	6	8
70	Proteomic and Metaproteomic Approaches to Understand Host-Microbe Interactions. <i>Analytical Chemistry</i> , <b>2018</b> , 90, 86-109	7.8	29
69	Metaproteomics reveals associations between microbiome and intestinal extracellular vesicle proteins in pediatric inflammatory bowel disease. <i>Nature Communications</i> , <b>2018</b> , 9, 2873	17.4	120
68	iMetaLab 1.0: a web platform for metaproteomics data analysis. <i>Bioinformatics</i> , <b>2018</b> , 34, 3954-3956	7.2	25
67	Separation and characterization of human microbiomes by metaproteomics. <i>TrAC - Trends in Analytical Chemistry</i> , <b>2018</b> , 108, 221-230	14.6	4

66	Proteomics Analysis of O-GalNAc Glycosylation in Human Serum by an Integrated Strategy. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 1469-1476	7.8	29
65	MetaLab: an automated pipeline for metaproteomic data analysis. <i>Microbiome</i> , <b>2017</b> , 5, 157	16.6	71
64	HISTONE DEACETYLASE6 Acts in Concert with Histone Methyltransferases SUVH4, SUVH5, and SUVH6 to Regulate Transposon Silencing. <i>Plant Cell</i> , <b>2017</b> , 29, 1970-1983	11.6	39
63	Zwitterionic Manganese and Gadolinium Metal-Organic Frameworks as Efficient Contrast Agents for in Vivo Magnetic Resonance Imaging. <i>ACS Applied Materials &amp; Interfaces</i> , <b>2017</b> , 9, 41378-41386	9.5	39
62	Salinity-Induced Palmella Formation Mechanism in Halotolerant Algae Revealed by Quantitative Proteomics and Phosphoproteomics. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 810	6.2	28
61	Plant Responses to Abiotic Stress Regulated by Histone Deacetylases. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 2147	6.2	53
60	Phosphoproteome Profiling Reveals Circadian Clock Regulation of Posttranslational Modifications in the Murine Hippocampus. <i>Frontiers in Neurology</i> , <b>2017</b> , 8, 110	4.1	19
59	Ultra-deep tyrosine phosphoproteomics enabled by a phosphotyrosine superbinder. <i>Nature Chemical Biology</i> , <b>2016</b> , 12, 959-966	11.7	88
58	N-Glycopeptide Reduction with Exoglycosidases Enables Accurate Characterization of Site-Specific N-Glycosylation. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 11837-11843	7.8	10
57	Bottom-Up Proteomics (2013-2015): Keeping up in the Era of Systems Biology. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 95-121	7.8	45
56	Characterization of site-specific glycosylation of secreted proteins associated with multi-drug resistance of gastric cancer. <i>Oncotarget</i> , <b>2016</b> , 7, 25315-27	3.3	31
55	Hybrid anisotropic nanostructures for dual-modal cancer imaging and image-guided chemo-thermo therapies. <i>Biomaterials</i> , <b>2016</b> , 103, 265-277	15.6	32
54	A bead-based cleavage method for large-scale identification of protease substrates. <i>Scientific Reports</i> , <b>2016</b> , 6, 22645	4.9	8
53	A peptide N-terminal protection strategy for comprehensive glycoproteome analysis using hydrazide chemistry based method. <i>Scientific Reports</i> , <b>2015</b> , 5, 10164	4.9	28
52	Highly Efficient Release of Glycopeptides from Hydrazide Beads by Hydroxylamine Assisted PNGase F Deglycosylation for N-Glycoproteome Analysis. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 10199-204	7.8	39
51	Specific Enrichment of Peptides with N-Terminal Serine/Threonine by a Solid-Phase Capture-Release Approach for Efficient Proteomics Analysis. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 11353-60	7.8	12
50	Fluorescence Imaging In Vivo at Wavelengths beyond 1500 nm. <i>Angewandte Chemie - International Edition</i> , <b>2015</b> , 54, 14758-62	16.4	231
49	Dragon fruit-like biocage as an iron trapping nanoplatfrom for high efficiency targeted cancer multimodality imaging. <i>Biomaterials</i> , <b>2015</b> , 69, 30-7	15.6	54

48	Magnetic nanoparticles coated with maltose-functionalized polyethyleneimine for highly efficient enrichment of N-glycopeptides. <i>Journal of Chromatography A</i> , <b>2015</b> , 1425, 213-20	4.5	34
47	Proteomic analysis of protein methylation in the yeast <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteomics</i> , <b>2015</b> , 114, 226-33	3.9	27
46	Drug Delivery: Engineering Melanin Nanoparticles as an Efficient Drug Delivery System for Imaging-Guided Chemotherapy (Adv. Mater. 34/2015). <i>Advanced Materials</i> , <b>2015</b> , 27, 5092-5092	24	4
45	Engineering Melanin Nanoparticles as an Efficient Drug-Delivery System for Imaging-Guided Chemotherapy. <i>Advanced Materials</i> , <b>2015</b> , 27, 5063-9	24	131
44	Fluorescence Imaging In Vivo at Wavelengths beyond 1500 nm. <i>Angewandte Chemie</i> , <b>2015</b> , 127, 14971-14975	14.875	72
43	High-sensitivity N-glycoproteomic analysis of mouse brain tissue by protein extraction with a mild detergent of N-dodecyl $\beta$ -D-maltoside. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 2054-7	7.8	20
42	Photoacoustic Imaging: Perylene-Diimide-Based Nanoparticles as Highly Efficient Photoacoustic Agents for Deep Brain Tumor Imaging in Living Mice (Adv. Mater. 5/2015). <i>Advanced Materials</i> , <b>2015</b> , 27, 774-774	24	4
41	Functionalizing with glycopeptide dendrimers significantly enhances the hydrophilicity of the magnetic nanoparticles. <i>Chemical Communications</i> , <b>2015</b> , 51, 4093-6	5.8	31
40	Large-scale quantification of single amino-acid variations by a variation-associated database search strategy. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 241-8	5.6	20
39	Trypsin-catalyzed N-terminal labeling of peptides with stable isotope-coded affinity tags for proteome analysis. <i>Analytical Chemistry</i> , <b>2014</b> , 86, 1170-7	7.8	8
38	An enzyme assisted RP-RPLC approach for in-depth analysis of human liver phosphoproteome. <i>Journal of Proteomics</i> , <b>2014</b> , 96, 253-62	3.9	166
37	Large-scale characterization of intact N-glycopeptides using an automated glycoproteomic method. <i>Journal of Proteomics</i> , <b>2014</b> , 110, 145-54	3.9	54
36	Quantitative proteomics reveals the kinetics of trypsin-catalyzed protein digestion. <i>Analytical and Bioanalytical Chemistry</i> , <b>2014</b> , 406, 6247-56	4.4	19
35	Integration of cell lysis, protein extraction, and digestion into one step for ultrafast sample preparation for phosphoproteome analysis. <i>Analytical Chemistry</i> , <b>2014</b> , 86, 6786-91	7.8	17
34	In situ sample processing approach (iSPA) for comprehensive quantitative phosphoproteome analysis. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 3896-904	5.6	12
33	Large-scale proteome quantification of hepatocellular carcinoma tissues by a three-dimensional liquid chromatography strategy integrated with sample preparation. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 3645-54	5.6	19
32	Differential analysis of N-glycoproteome between hepatocellular carcinoma and normal human liver tissues by combination of multiple protease digestion and solid phase based labeling. <i>Clinical Proteomics</i> , <b>2014</b> , 11, 26	5	6
31	Highly efficient N-glycoproteomic sample preparation by combining C(18) and graphitized carbon adsorbents. <i>Analytical and Bioanalytical Chemistry</i> , <b>2014</b> , 406, 3103-9	4.4	15

30	Comprehensive mapping of protein N-glycosylation in human liver by combining hydrophilic interaction chromatography and hydrazide chemistry. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 1713-21	5.6	61
29	Hybrid nanotrimers for dual T1 and T2-weighted magnetic resonance imaging. <i>ACS Nano</i> , <b>2014</b> , 8, 9884-9	6.7	91
28	Construction and validation of nano gold tripods for molecular imaging of living subjects. <i>Journal of the American Chemical Society</i> , <b>2014</b> , 136, 3560-71	16.4	144
27	Identification of chemoresistance-related cell-surface glycoproteins in leukemia cells and functional validation of candidate glycoproteins. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 1593-601	5.6	16
26	Ultrafast fluorescence imaging in vivo with conjugated polymer fluorophores in the second near-infrared window. <i>Nature Communications</i> , <b>2014</b> , 5, 4206	17.4	394
25	Identification of phosphopeptides with unknown cleavage specificity by a de novo sequencing assisted database search strategy. <i>Proteomics</i> , <b>2014</b> , 14, 2410-6	4.8	9
24	Protein digestion priority is independent of protein abundances. <i>Nature Methods</i> , <b>2014</b> , 11, 220-2	21.6	20
23	Cell nucleus targeting for living cell extraction of nucleic acid associated proteins with intracellular nanoprobes of magnetic carbon nanotubes. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 7038-43	7.8	28
22	A simple integrated system for rapid analysis of sialic-acid-containing N-glycopeptides from human serum. <i>Proteomics</i> , <b>2013</b> , 13, 1306-13	4.8	28
21	High specific phosphopeptides enrichment by titanium silicalite with post-treatment of desilication. <i>Analytical Methods</i> , <b>2013</b> , 5, 2939	3.2	5
20	A large-scale protein phosphorylation analysis reveals novel phosphorylation motifs and phosphoregulatory networks in Arabidopsis. <i>Journal of Proteomics</i> , <b>2013</b> , 78, 486-98	3.9	79
19	Analysis of human serum phosphopeptidome by a focused database searching strategy. <i>Journal of Proteomics</i> , <b>2013</b> , 78, 389-97	3.9	10
18	Monolithic capillary column based glycoproteomic reactor for high-sensitive analysis of N-glycoproteome. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 2847-52	7.8	50
17	N-Terminal Labeling of Peptides by Trypsin-Catalyzed Ligation for Quantitative Proteomics. <i>Angewandte Chemie</i> , <b>2013</b> , 125, 9375-9379	3.6	
16	N-terminal labeling of peptides by trypsin-catalyzed ligation for quantitative proteomics. <i>Angewandte Chemie - International Edition</i> , <b>2013</b> , 52, 9205-9	16.4	12
15	A six-plex proteome quantification strategy reveals the dynamics of protein turnover. <i>Scientific Reports</i> , <b>2013</b> , 3, 1827	4.9	11
14	Global screening of CK2 kinase substrates by an integrated phosphoproteomics workflow. <i>Scientific Reports</i> , <b>2013</b> , 3, 3460	4.9	61
13	Capture and dimethyl labeling of glycopeptides on hydrazide beads for quantitative glycoproteomics analysis. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 8452-6	7.8	40

12	A new method for quantitative analysis of cell surface glycoproteome. <i>Proteomics</i> , <b>2012</b> , 12, 3328-37	4.8	14
11	Centrifugation assisted microreactor enables facile integration of trypsin digestion, hydrophilic interaction chromatography enrichment, and on-column deglycosylation for rapid and sensitive N-glycoproteome analysis. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 5146-53	7.8	84
10	Improve the coverage for the analysis of phosphoproteome of HeLa cells by a tandem digestion approach. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 2828-37	5.6	44
9	Highly efficient extraction of cellular nucleic acid associated proteins in vitro with magnetic oxidized carbon nanotubes. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 10454-62	7.8	22
8	A comprehensive differential proteomic study of nitrate deprivation in Arabidopsis reveals complex regulatory networks of plant nitrogen responses. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 2301-15	5.6	58
7	Depletion of acidic phosphopeptides by SAX to improve the coverage for the detection of basophilic kinase substrates. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 4673-81	5.6	22
6	A proteomic analysis of engineered tendon formation under dynamic mechanical loading in vitro. <i>Biomaterials</i> , <b>2011</b> , 32, 4085-95	15.6	34
5	A bead-based approach for large-scale identification of in vitro kinase substrates. <i>Proteomics</i> , <b>2011</b> , 11, 4632-7	4.8	15
4	Perspectives of comprehensive phosphoproteome analysis using shotgun strategy. <i>Analytical Chemistry</i> , <b>2011</b> , 83, 8078-85	7.8	45
3	Improvement of the quantification accuracy and throughput for phosphoproteome analysis by a pseudo triplex stable isotope dimethyl labeling approach. <i>Analytical Chemistry</i> , <b>2011</b> , 83, 7755-62	7.8	51
2	ArMone: a software suite specially designed for processing and analysis of phosphoproteome data. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 2743-51	5.6	21
1	RapidAIM: A culture- and metaproteomics-based Rapid Assay of Individual Microbiome responses to drugs		2