

Rui-Jun Tian

List of Publications by Citations

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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.

90
papers

2,487
citations

29
h-index

47
g-index

101
ext. papers

2,935
ext. citations

7.3
avg, IF

4.68
L-index

#	Paper	IF	Citations
90	Large-scale phosphoproteome analysis of human liver tissue by enrichment and fractionation of phosphopeptides with strong anion exchange chromatography. <i>Proteomics</i> , 2008 , 8, 1346-61	4.8	180
89	Selective extraction of peptides from human plasma by highly ordered mesoporous silica particles for peptidome analysis. <i>Angewandte Chemie - International Edition</i> , 2007 , 46, 962-5	16.4	168
88	Targeting LIF-mediated paracrine interaction for pancreatic cancer therapy and monitoring. <i>Nature</i> , 2019 , 569, 131-135	50.4	155
87	Highly specific enrichment of phosphopeptides by zirconium dioxide nanoparticles for phosphoproteome analysis. <i>Electrophoresis</i> , 2007 , 28, 2201-15	3.6	132
86	Soluble FLT1 binds lipid microdomains in podocytes to control cell morphology and glomerular barrier function. <i>Cell</i> , 2012 , 151, 384-99	56.2	115
85	Ultrafast enzyme immobilization over large-pore nanoscale mesoporous silica particles. <i>Chemical Communications</i> , 2006 , 1322-4	5.8	107
84	Development of efficient protein extraction methods for shotgun proteome analysis of formalin-fixed tissues. <i>Journal of Proteome Research</i> , 2007 , 6, 1038-47	5.6	85
83	Simple and Integrated Spintip-Based Technology Applied for Deep Proteome Profiling. <i>Analytical Chemistry</i> , 2016 , 88, 4864-71	7.8	74
82	The highly selective capture of phosphopeptides by zirconium phosphonate-modified magnetic nanoparticles for phosphoproteome analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2008 , 19, 1176-86	3.5	61
81	Selective enrichment of endogenous peptides by chemically modified porous nanoparticles for peptidome analysis. <i>Journal of Chromatography A</i> , 2009 , 1216, 1270-8	4.5	56
80	Deep Metaproteomics Approach for the Study of Human Microbiomes. <i>Analytical Chemistry</i> , 2017 , 89, 9407-9415	7.8	54
79	Rare cell proteomic reactor applied to stable isotope labeling by amino acids in cell culture (SILAC)-based quantitative proteomics study of human embryonic stem cell differentiation. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.000679	7.6	50
78	Preparation of monolithic silica column with strong cation-exchange stationary phase for capillary electrochromatography. <i>Journal of Separation Science</i> , 2005 , 28, 751-6	3.4	48
77	Large-pore mesoporous SBA-15 silica particles with submicrometer size as stationary phases for high-speed CEC separation. <i>Electrophoresis</i> , 2006 , 27, 742-8	3.6	47
76	Electrochromatographic evaluation of a silica monolith capillary column for separation of basic pharmaceuticals. <i>Electrophoresis</i> , 2005 , 26, 790-7	3.6	47
75	Combinatorial proteomic analysis of intercellular signaling applied to the CD28 T-cell costimulatory receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E1594-603	11.5	44
74	Advances in chromatographic techniques and methods in shotgun proteome analysis. <i>TrAC - Trends in Analytical Chemistry</i> , 2007 , 26, 80-84	14.6	44

73	High throughput and accurate serum proteome profiling by integrated sample preparation technology and single-run data independent mass spectrometry analysis. <i>Journal of Proteomics</i> , 2018 , 174, 9-16	3.9	40
72	Proteomics: from technology developments to biological applications. <i>Analytical Chemistry</i> , 2009 , 81, 4585-99	7.8	40
71	Capillary electrochromatography with a neutral monolithic column for classification of analytes and determination of basic drugs in human serum. <i>Electrophoresis</i> , 2005 , 26, 3452-9	3.6	36
70	Identification, Quantification, and Site Localization of Protein Posttranslational Modifications via Mass Spectrometry-Based Proteomics. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 919, 345-382	3.6	36
69	Automation of nanoflow liquid chromatography-tandem mass spectrometry for proteome analysis by using a strong cation exchange trap column. <i>Proteomics</i> , 2007 , 7, 528-539	4.8	35
68	Characterization of small-moleculeBiomacromolecule interactions: From simple to complex. <i>TrAC - Trends in Analytical Chemistry</i> , 2005 , 24, 810-825	14.6	35
67	Chimeric Antigen Receptor Designed to Prevent Ubiquitination and Downregulation Showed Durable Antitumor Efficacy. <i>Immunity</i> , 2020 , 53, 456-470.e6	32.3	35
66	Sequence-specific recognition of a PxLPxI/L motif by an ankyrin repeat tumbler lock. <i>Science Signaling</i> , 2012 , 5, ra39	8.8	33
65	Development of a multiplexed microfluidic proteomic reactor and its application for studying protein-protein interactions. <i>Analytical Chemistry</i> , 2011 , 83, 4095-102	7.8	32
64	Selective extraction of peptides in acidic human plasma by porous silica nanoparticles for peptidome analysis with 2-D LC-MS/MS. <i>Journal of Separation Science</i> , 2007 , 30, 2204-9	3.4	32
63	A novel whole-cell lysate kinase assay identifies substrates of the p38 MAPK in differentiating myoblasts. <i>Skeletal Muscle</i> , 2012 , 2, 5	5.1	30
62	Hybrid silica monolithic column for capillary electrochromatography with enhanced cathodic electroosmotic flow. <i>Electrophoresis</i> , 2006 , 27, 4266-72	3.6	30
61	Kindlin-2 Association with Rho GDP-Dissociation Inhibitor Suppresses Rac1 Activation and Podocyte Injury. <i>Journal of the American Society of Nephrology: JASN</i> , 2017 , 28, 3545-3562	12.7	29
60	Selective Extraction of Peptides from Human Plasma by Highly Ordered Mesoporous Silica Particles for Peptidome Analysis. <i>Angewandte Chemie</i> , 2007 , 119, 980-983	3.6	27
59	Analysis of the subcellular phosphoproteome using a novel phosphoproteomic reactor. <i>Journal of Proteome Research</i> , 2010 , 9, 1279-88	5.6	25
58	Uncovering the proteome response of the master circadian clock to light using an AutoProteome system. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.007252	7.6	24
57	Separation of basic and acidic compounds by capillary electrochromatography using monolithic silica capillary columns with zwitterionic stationary phase. <i>Journal of Separation Science</i> , 2007 , 30, 891-9	3.4	23
56	Spatial-Resolution Cell Type Proteome Profiling of Cancer Tissue by Fully Integrated Proteomics Technology. <i>Analytical Chemistry</i> , 2018 , 90, 5879-5886	7.8	20

55	Mitosis-specific acetylation tunes Ran effector binding for chromosome segregation. <i>Journal of Molecular Cell Biology</i> , 2018 , 10, 18-32	6.3	20
54	Automated injection of uncleaned samples using a ten-port switching valve and a strong cation-exchange trap column for proteome analysis. <i>Journal of Chromatography A</i> , 2007 , 1171, 56-62	4.5	20
53	Phosphorylation of the Bin, Amphiphysin, and RSV161/167 (BAR) domain of ACAP4 regulates membrane tubulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 11023-8	11.5	19
52	Integrated proteomics sample preparation and fractionation: Method development and applications. <i>TrAC - Trends in Analytical Chemistry</i> , 2019 , 120, 115667	14.6	18
51	Evolution of Nucleic Acid Aptamers Capable of Specifically Targeting Glioma Stem Cells via Cell-SELEX. <i>Analytical Chemistry</i> , 2019 , 91, 8070-8077	7.8	18
50	3D-SISPROT: A simple and integrated spintip-based protein digestion and three-dimensional peptide fractionation technology for deep proteome profiling. <i>Journal of Chromatography A</i> , 2017 , 1498, 207-214	4.5	17
49	Acetylation of ACAP4 regulates CCL18-elicited breast cancer cell migration and invasion. <i>Journal of Molecular Cell Biology</i> , 2018 , 10, 559-572	6.3	17
48	Mixed-mode ion exchange-based integrated proteomics technology for fast and deep plasma proteome profiling. <i>Journal of Chromatography A</i> , 2018 , 1564, 76-84	4.5	16
47	Bruton's tyrosine kinase potentiates ALK signaling and serves as a potential therapeutic target of neuroblastoma. <i>Oncogene</i> , 2018 , 37, 6180-6194	9.2	15
46	Chemical proteomic study of isoprenoid chain interactome with a synthetic photoaffinity probe. <i>Proteomics</i> , 2008 , 8, 3094-104	4.8	15
45	Analysis of low-abundance proteins using the proteomic reactor with pH fractionation. <i>Talanta</i> , 2010 , 80, 1526-31	6.2	14
44	Biological fingerprinting analysis of the interactome of a kinase inhibitor in human plasma by a chemproteomic approach. <i>Journal of Chromatography A</i> , 2006 , 1134, 134-42	4.5	14
43	Exploring intercellular signaling by proteomic approaches. <i>Proteomics</i> , 2014 , 14, 498-512	4.8	13
42	CaMKII-driven, phosphatase-checked postsynaptic plasticity via phase separation. <i>Cell Research</i> , 2021 , 31, 37-51	24.7	13
41	Fast quantitative urinary proteomic profiling workflow for biomarker discovery in kidney cancer. <i>Clinical Proteomics</i> , 2018 , 15, 42	5	13
40	An integrated strategy for highly sensitive phosphoproteome analysis from low micrograms of protein samples. <i>Analyst, The</i> , 2018 , 143, 3693-3701	5	12
39	MST4 kinase phosphorylates ACAP4 protein to orchestrate apical membrane remodeling during gastric acid secretion. <i>Journal of Biological Chemistry</i> , 2017 , 292, 16174-16187	5.4	12
38	Improvement of performance in label-free quantitative proteome analysis with monolithic electrospray ionization emitter. <i>Journal of Separation Science</i> , 2008 , 31, 2589-97	3.4	12

37	Spatiotemporal profiling of cytosolic signaling complexes in living cells by selective proximity proteomics. <i>Nature Communications</i> , 2021 , 12, 71	17.4	12
36	Integrated and Quantitative Proteomic Approach for Charting Temporal and Endogenous Protein Complexes. <i>Analytical Chemistry</i> , 2018 , 90, 12574-12583	7.8	12
35	Spatial proteome profiling by immunohistochemistry-based laser capture microdissection and data-independent acquisition proteomics. <i>Analytica Chimica Acta</i> , 2020 , 1127, 140-148	6.6	10
34	Phosphorylation of PP1 Regulator Sds22 by PLK1 Ensures Accurate Chromosome Segregation. <i>Journal of Biological Chemistry</i> , 2016 , 291, 21123-21136	5.4	10
33	A Fully Integrated Spintip-Based Approach for Sensitive and Quantitative Profiling of Region-Resolved in Vivo Brain Glycoproteome. <i>Analytical Chemistry</i> , 2019 , 91, 9181-9189	7.8	9
32	An enhanced chemically defined SILAC culture system for quantitative proteomics study of human embryonic stem cells. <i>Proteomics</i> , 2011 , 11, 4040-6	4.8	9
31	An integrated strategy for high-sensitive and multi-level glycoproteome analysis from low micrograms of protein samples. <i>Journal of Chromatography A</i> , 2019 , 1600, 46-54	4.5	8
30	Facile synthesis of carboxymethyl- β -cyclodextrin conjugated magnetic nanoparticles for selective enrichment of glycopeptides. <i>Rapid Communications in Mass Spectrometry</i> , 2016 , 30 Suppl 1, 190-5	2.2	8
29	Mutational Analysis of Glycogen Synthase Kinase 3 β Protein Kinase Together with Kinome-Wide Binding and Stability Studies Suggests Context-Dependent Recognition of Kinases by the Chaperone Heat Shock Protein 90. <i>Molecular and Cellular Biology</i> , 2016 , 36, 1007-18	4.8	8
28	CoreFlow: a computational platform for integration, analysis and modeling of complex biological data. <i>Journal of Proteomics</i> , 2014 , 100, 167-73	3.9	8
27	Rapid and sensitive MRM-based mass spectrometry approach for systematically exploring ganglioside-protein interactions. <i>Proteomics</i> , 2013 , 13, 1334-8	4.8	8
26	AutoProteome Chip System for Fully Automated and Integrated Proteomics Sample Preparation and Peptide Fractionation. <i>Analytical Chemistry</i> , 2020 , 92, 8893-8900	7.8	7
25	Photoaffinity-engineered protein scaffold for systematically exploring native phosphotyrosine signaling complexes in tumor samples. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E8863-E8872	11.5	7
24	Time-of-day- and light-dependent expression of ubiquitin protein ligase E3 component N-recogin 4 (UBR4) in the suprachiasmatic nucleus circadian clock. <i>PLoS ONE</i> , 2014 , 9, e103103	3.7	6
23	Synergistic optimization of Liquid Chromatography and Mass Spectrometry parameters on Orbitrap Tribrid mass spectrometer for high efficient data-dependent proteomics. <i>Journal of Mass Spectrometry</i> , 2021 , 56, e4653	2.2	6
22	Combinatory Data-Independent Acquisition and Parallel Reaction Monitoring Method for Deep Profiling of Gangliosides. <i>Analytical Chemistry</i> , 2020 , 92, 10830-10838	7.8	5
21	Dynamic crotonylation of EB1 by TIP60 ensures accurate spindle positioning in mitosis. <i>Nature Chemical Biology</i> , 2021 , 17, 1314-1323	11.7	5
20	Spatial proteomics for understanding the tissue microenvironment. <i>Analyst, The</i> , 2021 , 146, 3777-3798	5	5

19	A robust and scalable active-matrix driven digital microfluidic platform based on printed-circuit board technology. <i>Lab on A Chip</i> , 2021 , 21, 1886-1896	7.2	5
18	Proteomic Analysis of Secreted Proteins from Cell Microenvironment. <i>Methods in Molecular Biology</i> , 2017 , 1662, 45-58	1.4	4
17	High-Throughput and Integrated Chemical Proteomic Approach for Profiling Phosphotyrosine Signaling Complexes. <i>Analytical Chemistry</i> , 2020 , 92, 8933-8942	7.8	3
16	Phosphorylation-regulated HMGA1a-P53 interaction unveils the function of HMGA1a acidic tail phosphorylations via synthetic proteins. <i>Cell Chemical Biology</i> , 2021 , 28, 722-732.e8	8.2	3
15	Mass Spectrometry-Based Protein Complex Profiling in Time and Space. <i>Analytical Chemistry</i> , 2021 , 93, 598-619	7.8	3
14	Fully Integrated and Multiplexed Sample Preparation Technology for Sensitive Interactome Profiling. <i>Analytical Chemistry</i> , 2021 , 93, 3026-3034	7.8	3
13	SH2 Domains as Affinity Reagents for Phosphotyrosine Protein Enrichment and Proteomic Analysis. <i>Methods in Molecular Biology</i> , 2017 , 1555, 395-406	1.4	2
12	High-Throughput Phosphotyrosine Protein Complexes Screening by Photoaffinity-Engineered Protein Scaffold-Based Forward-Phase Protein Array. <i>Analytical Chemistry</i> , 2019 , 91, 10026-10032	7.8	2
11	Progress and Application of LC-MS Technologies for Characterizing Protein Post Translational Modifications. <i>Chinese Journal of Analytical Chemistry</i> , 2015 , 43, 1479-1489	1.6	2
10	OPA-Based Bifunctional Linker for Protein Labeling and Profiling. <i>Biochemistry</i> , 2020 , 59, 175-178	3.2	2
9	Feedback control of PLK1 by Apolo1 ensures accurate chromosome segregation. <i>Cell Reports</i> , 2021 , 36, 109343	10.6	2
8	Combinatory strategy using nanoscale proteomics and machine learning for T cell subtyping in peripheral blood of single multiple myeloma patients. <i>Analytica Chimica Acta</i> , 2021 , 1173, 338672	6.6	2
7	Combining Metabolic Alkyne Labeling and Click Chemistry for Secretome Analysis of Serum-Containing Conditioned Medium. <i>Chinese Journal of Chemistry</i> , 2021 , 39, 1843-1848	4.9	1
6	Dissecting the multi-omics atlas of the exosomes released by human lung adenocarcinoma stem-like cells. <i>Npj Genomic Medicine</i> , 2021 , 6, 48	6.2	1
5	Multioomic analysis of a dried single-drop plasma sample using an integrated mass spectrometry approach. <i>Analyst, The</i> , 2020 , 145, 6441-6446	5	0
4	Stable and EGF-Induced Temporal Interactome Profiling of CBL and CBLB Highlights Their Signaling Complex Diversity. <i>Journal of Proteome Research</i> , 2021 , 20, 3709-3719	5.6	0
3	Fritted tip capillary column with negligible dead volume facilitated ultrasensitive and deep proteomics.. <i>Analytica Chimica Acta</i> , 2022 , 1201, 339615	6.6	0
2	Mass spectrometry-based ganglioside profiling provides potential insights into Alzheimer's disease development. <i>Journal of Chromatography A</i> , 2022 , 463196	4.5	0

- 1 Zwitter-ionic Monolith-based Spintip Column Coupled with Evosep One Liquid Chromatography for High-throughput Proteomic Analysis. *Journal of Chromatography A*, **2022**, 463122 4·5