

# Rui-Jun Tian

## 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.

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	Fritted tip capillary column with negligible dead volume facilitated ultrasensitive and deep proteomics.. <i>Analytica Chimica Acta</i> , <b>2022</b> , 1201, 339615	6.6	0
89	Zwitter-ionic Monolith-based Spintip Column Coupled with Evosep One Liquid Chromatography for High-throughput Proteomic Analysis. <i>Journal of Chromatography A</i> , <b>2022</b> , 463122	4.5	
88	Mass spectrometry-based ganglioside profiling provides potential insights into Alzheimer's disease development. <i>Journal of Chromatography A</i> , <b>2022</b> , 463196	4.5	0
87	Dynamic crotonylation of EB1 by TIP60 ensures accurate spindle positioning in mitosis. <i>Nature Chemical Biology</i> , <b>2021</b> , 17, 1314-1323	11.7	5
86	Combining Metabolic Alkyne Labeling and Click Chemistry for Secretome Analysis of Serum-Containing Conditioned Medium. <i>Chinese Journal of Chemistry</i> , <b>2021</b> , 39, 1843-1848	4.9	1
85	Phosphorylation-regulated HMGA1a-P53 interaction unveils the function of HMGA1a acidic tail phosphorylations via synthetic proteins. <i>Cell Chemical Biology</i> , <b>2021</b> , 28, 722-732.e8	8.2	3
84	Dissecting the multi-omics atlas of the exosomes released by human lung adenocarcinoma stem-like cells. <i>Npj Genomic Medicine</i> , <b>2021</b> , 6, 48	6.2	1
83	Stable and EGF-Induced Temporal Interactome Profiling of CBL and CBLB Highlights Their Signaling Complex Diversity. <i>Journal of Proteome Research</i> , <b>2021</b> , 20, 3709-3719	5.6	0
82	Feedback control of PLK1 by Apolo1 ensures accurate chromosome segregation. <i>Cell Reports</i> , <b>2021</b> , 36, 109343	10.6	2
81	Mass Spectrometry-Based Protein Complex Profiling in Time and Space. <i>Analytical Chemistry</i> , <b>2021</b> , 93, 598-619	7.8	3
80	CaMKII-driven, phosphatase-checked postsynaptic plasticity via phase separation. <i>Cell Research</i> , <b>2021</b> , 31, 37-51	24.7	13
79	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> , <b>2021</b> , 56, e4653	2.2	6
78	Spatial proteomics for understanding the tissue microenvironment. <i>Analyst, The</i> , <b>2021</b> , 146, 3777-3798	5	5
77	A robust and scalable active-matrix driven digital microfluidic platform based on printed-circuit board technology. <i>Lab on A Chip</i> , <b>2021</b> , 21, 1886-1896	7.2	5
76	Spatiotemporal profiling of cytosolic signaling complexes in living cells by selective proximity proteomics. <i>Nature Communications</i> , <b>2021</b> , 12, 71	17.4	12
75	Fully Integrated and Multiplexed Sample Preparation Technology for Sensitive Interactome Profiling. <i>Analytical Chemistry</i> , <b>2021</b> , 93, 3026-3034	7.8	3
74	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> , <b>2021</b> , 1173, 338672	6.6	2

73	AutoProteome Chip System for Fully Automated and Integrated Proteomics Sample Preparation and Peptide Fractionation. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 8893-8900	7.8	7
72	High-Throughput and Integrated Chemical Proteomic Approach for Profiling Phosphotyrosine Signaling Complexes. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 8933-8942	7.8	3
71	Spatial proteome profiling by immunohistochemistry-based laser capture microdissection and data-independent acquisition proteomics. <i>Analytica Chimica Acta</i> , <b>2020</b> , 1127, 140-148	6.6	10
70	Combinatory Data-Independent Acquisition and Parallel Reaction Monitoring Method for Deep Profiling of Gangliosides. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 10830-10838	7.8	5
69	OPA-Based Bifunctional Linker for Protein Labeling and Profiling. <i>Biochemistry</i> , <b>2020</b> , 59, 175-178	3.2	2
68	Chimeric Antigen Receptor Designed to Prevent Ubiquitination and Downregulation Showed Durable Antitumor Efficacy. <i>Immunity</i> , <b>2020</b> , 53, 456-470.e6	32.3	35
67	Multiomic analysis of a dried single-drop plasma sample using an integrated mass spectrometry approach. <i>Analyst, The</i> , <b>2020</b> , 145, 6441-6446	5	0
66	Integrated proteomics sample preparation and fractionation: Method development and applications. <i>TrAC - Trends in Analytical Chemistry</i> , <b>2019</b> , 120, 115667	14.6	18
65	A Fully Integrated Spintip-Based Approach for Sensitive and Quantitative Profiling of Region-Resolved in Vivo Brain Glycoproteome. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 9181-9189	7.8	9
64	Evolution of Nucleic Acid Aptamers Capable of Specifically Targeting Glioma Stem Cells via Cell-SELEX. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 8070-8077	7.8	18
63	An integrated strategy for high-sensitive and multi-level glycoproteome analysis from low micrograms of protein samples. <i>Journal of Chromatography A</i> , <b>2019</b> , 1600, 46-54	4.5	8
62	Targeting LIF-mediated paracrine interaction for pancreatic cancer therapy and monitoring. <i>Nature</i> , <b>2019</b> , 569, 131-135	50.4	155
61	High-Throughput Phosphotyrosine Protein Complexes Screening by Photoaffinity-Engineered Protein Scaffold-Based Forward-Phase Protein Array. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 10026-10032	7.8	2
60	Spatial-Resolution Cell Type Proteome Profiling of Cancer Tissue by Fully Integrated Proteomics Technology. <i>Analytical Chemistry</i> , <b>2018</b> , 90, 5879-5886	7.8	20
59	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> , <b>2018</b> , 174, 9-16	3.9	40
58	Mitosis-specific acetylation tunes Ran effector binding for chromosome segregation. <i>Journal of Molecular Cell Biology</i> , <b>2018</b> , 10, 18-32	6.3	20
57	Bruton's tyrosine kinase potentiates ALK signaling and serves as a potential therapeutic target of neuroblastoma. <i>Oncogene</i> , <b>2018</b> , 37, 6180-6194	9.2	15
56	An integrated strategy for highly sensitive phosphoproteome analysis from low micrograms of protein samples. <i>Analyst, The</i> , <b>2018</b> , 143, 3693-3701	5	12

55	Acetylation of ACAP4 regulates CCL18-elicited breast cancer cell migration and invasion. <i>Journal of Molecular Cell Biology</i> , <b>2018</b> , 10, 559-572	6.3	17
54	Fast quantitative urinary proteomic profiling workflow for biomarker discovery in kidney cancer. <i>Clinical Proteomics</i> , <b>2018</b> , 15, 42	5	13
53	Integrated and Quantitative Proteomic Approach for Charting Temporal and Endogenous Protein Complexes. <i>Analytical Chemistry</i> , <b>2018</b> , 90, 12574-12583	7.8	12
52	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> , <b>2018</b> , 115, E8863-E8872	11.5	7
51	Mixed-mode ion exchange-based integrated proteomics technology for fast and deep plasma proteome profiling. <i>Journal of Chromatography A</i> , <b>2018</b> , 1564, 76-84	4.5	16
50	SH2 Domains as Affinity Reagents for Phosphotyrosine Protein Enrichment and Proteomic Analysis. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1555, 395-406	1.4	2
49	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> , <b>2017</b> , 1498, 207-214	4.5	17
48	Proteomic Analysis of Secreted Proteins from Cell Microenvironment. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1662, 45-58	1.4	4
47	Deep Metaproteomics Approach for the Study of Human Microbiomes. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 9407-9415	7.8	54
46	Kindlin-2 Association with Rho GDP-Dissociation Inhibitor Suppresses Rac1 Activation and Podocyte Injury. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2017</b> , 28, 3545-3562	12.7	29
45	MST4 kinase phosphorylates ACAP4 protein to orchestrate apical membrane remodeling during gastric acid secretion. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 16174-16187	5.4	12
44	Facile synthesis of carboxymethyl- $\beta$ -cyclodextrin conjugated magnetic nanoparticles for selective enrichment of glycopeptides. <i>Rapid Communications in Mass Spectrometry</i> , <b>2016</b> , 30 Suppl 1, 190-5	2.2	8
43	Mutational Analysis of Glycogen Synthase Kinase 3 $\beta$ 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> , <b>2016</b> , 36, 1007-18	4.8	8
42	Identification, Quantification, and Site Localization of Protein Posttranslational Modifications via Mass Spectrometry-Based Proteomics. <i>Advances in Experimental Medicine and Biology</i> , <b>2016</b> , 919, 345-382	2.6	36
41	Simple and Integrated Spintip-Based Technology Applied for Deep Proteome Profiling. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 4864-71	7.8	74
40	Phosphorylation of PP1 Regulator Sds22 by PLK1 Ensures Accurate Chromosome Segregation. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 21123-21136	5.4	10
39	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> , <b>2015</b> , 112, E1594-603	11.5	44
38	Progress and Application of LC-MS Technologies for Characterizing Protein Post Translational Modifications. <i>Chinese Journal of Analytical Chemistry</i> , <b>2015</b> , 43, 1479-1489	1.6	2

37	CoreFlow: a computational platform for integration, analysis and modeling of complex biological data. <i>Journal of Proteomics</i> , <b>2014</b> , 100, 167-73	3.9	8
36	Exploring intercellular signaling by proteomic approaches. <i>Proteomics</i> , <b>2014</b> , 14, 498-512	4.8	13
35	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> , <b>2014</b> , 9, e103103	3.7	6
34	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> , <b>2013</b> , 110, 11023-8	11.5	19
33	Rapid and sensitive MRM-based mass spectrometry approach for systematically exploring ganglioside-protein interactions. <i>Proteomics</i> , <b>2013</b> , 13, 1334-8	4.8	8
32	Soluble FLT1 binds lipid microdomains in podocytes to control cell morphology and glomerular barrier function. <i>Cell</i> , <b>2012</b> , 151, 384-99	56.2	115
31	Sequence-specific recognition of a PxLPxI/L motif by an ankyrin repeat tumbler lock. <i>Science Signaling</i> , <b>2012</b> , 5, ra39	8.8	33
30	A novel whole-cell lysate kinase assay identifies substrates of the p38 MAPK in differentiating myoblasts. <i>Skeletal Muscle</i> , <b>2012</b> , 2, 5	5.1	30
29	An enhanced chemically defined SILAC culture system for quantitative proteomics study of human embryonic stem cells. <i>Proteomics</i> , <b>2011</b> , 11, 4040-6	4.8	9
28	Development of a multiplexed microfluidic proteomic reactor and its application for studying protein-protein interactions. <i>Analytical Chemistry</i> , <b>2011</b> , 83, 4095-102	7.8	32
27	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> , <b>2011</b> , 10, M110.000679	7.6	50
26	Uncovering the proteome response of the master circadian clock to light using an AutoProteome system. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, M110.007252	7.6	24
25	Analysis of the subcellular phosphoproteome using a novel phosphoproteomic reactor. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 1279-88	5.6	25
24	Analysis of low-abundance proteins using the proteomic reactor with pH fractionation. <i>Talanta</i> , <b>2010</b> , 80, 1526-31	6.2	14
23	Selective enrichment of endogenous peptides by chemically modified porous nanoparticles for peptidome analysis. <i>Journal of Chromatography A</i> , <b>2009</b> , 1216, 1270-8	4.5	56
22	Proteomics: from technology developments to biological applications. <i>Analytical Chemistry</i> , <b>2009</b> , 81, 4585-99	7.8	40
21	Large-scale phosphoproteome analysis of human liver tissue by enrichment and fractionation of phosphopeptides with strong anion exchange chromatography. <i>Proteomics</i> , <b>2008</b> , 8, 1346-61	4.8	180
20	Chemical proteomic study of isoprenoid chain interactome with a synthetic photoaffinity probe. <i>Proteomics</i> , <b>2008</b> , 8, 3094-104	4.8	15

19	Improvement of performance in label-free quantitative proteome analysis with monolithic electrospray ionization emitter. <i>Journal of Separation Science</i> , <b>2008</b> , 31, 2589-97	3.4	12
18	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> , <b>2008</b> , 19, 1176-86	3.5	61
17	Development of efficient protein extraction methods for shotgun proteome analysis of formalin-fixed tissues. <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 1038-47	5.6	85
16	Selective extraction of peptides from human plasma by highly ordered mesoporous silica particles for peptidome analysis. <i>Angewandte Chemie - International Edition</i> , <b>2007</b> , 46, 962-5	16.4	168
15	Selective Extraction of Peptides from Human Plasma by Highly Ordered Mesoporous Silica Particles for Peptidome Analysis. <i>Angewandte Chemie</i> , <b>2007</b> , 119, 980-983	3.6	27
14	Highly specific enrichment of phosphopeptides by zirconium dioxide nanoparticles for phosphoproteome analysis. <i>Electrophoresis</i> , <b>2007</b> , 28, 2201-15	3.6	132
13	Separation of basic and acidic compounds by capillary electrochromatography using monolithic silica capillary columns with zwitterionic stationary phase. <i>Journal of Separation Science</i> , <b>2007</b> , 30, 891-9	3.4	23
12	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> , <b>2007</b> , 30, 2204-9	3.4	32
11	Advances in chromatographic techniques and methods in shotgun proteome analysis. <i>TrAC - Trends in Analytical Chemistry</i> , <b>2007</b> , 26, 80-84	14.6	44
10	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> , <b>2007</b> , 1171, 56-62	4.5	20
9	Automation of nanoflow liquid chromatography-tandem mass spectrometry for proteome analysis by using a strong cation exchange trap column. <i>Proteomics</i> , <b>2007</b> , 7, 528-539	4.8	35
8	Large-pore mesoporous SBA-15 silica particles with submicrometer size as stationary phases for high-speed CEC separation. <i>Electrophoresis</i> , <b>2006</b> , 27, 742-8	3.6	47
7	Hybrid silica monolithic column for capillary electrochromatography with enhanced cathodic electroosmotic flow. <i>Electrophoresis</i> , <b>2006</b> , 27, 4266-72	3.6	30
6	Biological fingerprinting analysis of the interactome of a kinase inhibitor in human plasma by a chemoproteomic approach. <i>Journal of Chromatography A</i> , <b>2006</b> , 1134, 134-42	4.5	14
5	Ultrafast enzyme immobilization over large-pore nanoscale mesoporous silica particles. <i>Chemical Communications</i> , <b>2006</b> , 1322-4	5.8	107
4	Characterization of small-moleculeBiomacromolecule interactions: From simple to complex. <i>TrAC - Trends in Analytical Chemistry</i> , <b>2005</b> , 24, 810-825	14.6	35
3	Electrochromatographic evaluation of a silica monolith capillary column for separation of basic pharmaceuticals. <i>Electrophoresis</i> , <b>2005</b> , 26, 790-7	3.6	47
2	Capillary electrochromatography with a neutral monolithic column for classification of analytes and determination of basic drugs in human serum. <i>Electrophoresis</i> , <b>2005</b> , 26, 3452-9	3.6	36

- 1 Preparation of monolithic silica column with strong cation-exchange stationary phase for capillary electrochromatography. *Journal of Separation Science*, **2005**, 28, 751-6 3·4 4<sup>8</sup>