

Rui-Jun Tian

List of Publications by Year in descending order

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95
papers

3,341
citations

147566

31
h-index

168136

53
g-index

101
all docs

101
docs citations

101
times ranked

4559
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting LIF-mediated paracrine interaction for pancreatic cancer therapy and monitoring. <i>Nature</i> , 2019, 569, 131-135.	13.7	287
2	Large-scale phosphoproteome analysis of human liver tissue by enrichment and fractionation of phosphopeptides with strong anion exchange chromatography. <i>Proteomics</i> , 2008, 8, 1346-1361.	1.3	192
3	Selective Extraction of Peptides from Human Plasma by Highly Ordered Mesoporous Silica Particles for Peptidome Analysis. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 962-965.	7.2	174
4	Soluble FLT1 Binds Lipid Microdomains in Podocytes to Control Cell Morphology and Glomerular Barrier Function. <i>Cell</i> , 2012, 151, 384-399.	13.5	144
5	Highly specific enrichment of phosphopeptides by zirconium dioxide nanoparticles for phosphoproteome analysis. <i>Electrophoresis</i> , 2007, 28, 2201-2215.	1.3	137
6	Ultrafast enzyme immobilization over large-pore nanoscale mesoporous silica particles. <i>Chemical Communications</i> , 2006, , 1322.	2.2	112
7	Simple and Integrated Spintip-Based Technology Applied for Deep Proteome Profiling. <i>Analytical Chemistry</i> , 2016, 88, 4864-4871.	3.2	107
8	Development of Efficient Protein Extraction Methods for Shotgun Proteome Analysis of Formalin-Fixed Tissues. <i>Journal of Proteome Research</i> , 2007, 6, 1038-1047.	1.8	92
9	Deep Metaproteomics Approach for the Study of Human Microbiomes. <i>Analytical Chemistry</i> , 2017, 89, 9407-9415.	3.2	83
10	Chimeric Antigen Receptor Designed to Prevent Ubiquitination and Downregulation Showed Durable Antitumor Efficacy. <i>Immunity</i> , 2020, 53, 456-470.e6.	6.6	83
11	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.	1.2	66
12	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.	3.3	65
13	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, 1176-1186.	1.2	64
14	Selective enrichment of endogenous peptides by chemically modified porous nanoparticles for peptidome analysis. <i>Journal of Chromatography A</i> , 2009, 1216, 1270-1278.	1.8	59
15	Large-pore mesoporous SBA-15 silica particles with submicrometer size as stationary phases for high-speed CEC separation. <i>Electrophoresis</i> , 2006, 27, 742-748.	1.3	52
16	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, S1-S10.	2.5	52
17	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.	0.8	51
18	Electrochromatographic evaluation of a silica monolith capillary column for separation of basic pharmaceuticals. <i>Electrophoresis</i> , 2005, 26, 790-797.	1.3	49

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19	Preparation of monolithic silica column with strong cation-exchange stationary phase for capillary electrochromatography. <i>Journal of Separation Science</i> , 2005, 28, 751-756.	1.3	48
20	Advances in chromatographic techniques and methods in shotgun proteome analysis. <i>TrAC - Trends in Analytical Chemistry</i> , 2007, 26, 80-84.	5.8	47
21	A novel whole-cell lysate kinase assay identifies substrates of the p38 MAPK in differentiating myoblasts. <i>Skeletal Muscle</i> , 2012, 2, 5.	1.9	43
22	Spatiotemporal profiling of cytosolic signaling complexes in living cells by selective proximity proteomics. <i>Nature Communications</i> , 2021, 12, 71.	5.8	43
23	Proteomics: From Technology Developments to Biological Applications. <i>Analytical Chemistry</i> , 2009, 81, 4585-4599.	3.2	42
24	Sequence-Specific Recognition of a PxLPxI/L Motif by an Ankyrin Repeat Tumbler Lock. <i>Science Signaling</i> , 2012, 5, ra39.	1.6	42
25	Characterization of small-molecule-biomacromolecule interactions: From simple to complex. <i>TrAC - Trends in Analytical Chemistry</i> , 2005, 24, 810-825.	5.8	39
26	CaMKII β -driven, phosphatase-checked postsynaptic plasticity via phase separation. <i>Cell Research</i> , 2021, 31, 37-51.	5.7	39
27	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.	1.3	38
28	Kindlin-2 Association with Rho GDP-Dissociation Inhibitor β Suppresses Rac1 Activation and Podocyte Injury. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 3545-3562.	3.0	38
29	Capillary electrochromatography with a neutral monolithic column for classification of analytes and determination of basic drugs in human serum. <i>Electrophoresis</i> , 2005, 26, 3452-3459.	1.3	36
30	Selective extraction of peptides in acidic human plasma by porous silica nanoparticles for peptidome analysis with 2D LC-MS/MS. <i>Journal of Separation Science</i> , 2007, 30, 2204-2209.	1.3	35
31	Spatial-Resolution Cell Type Proteome Profiling of Cancer Tissue by Fully Integrated Proteomics Technology. <i>Analytical Chemistry</i> , 2018, 90, 5879-5886.	3.2	35
32	Development of a Multiplexed Microfluidic Proteomic Reactor and Its Application for Studying Protein-Protein Interactions. <i>Analytical Chemistry</i> , 2011, 83, 4095-4102.	3.2	34
33	Integrated proteomics sample preparation and fractionation: Method development and applications. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 120, 115667.	5.8	33
34	Mitosis-specific acetylation tunes Ran effector binding for chromosome segregation. <i>Journal of Molecular Cell Biology</i> , 2018, 10, 18-32.	1.5	32
35	Hybrid silica monolithic column for capillary electrochromatography with enhanced cathodic electroosmotic flow. <i>Electrophoresis</i> , 2006, 27, 4266-4272.	1.3	31
36	Dynamic crotonylation of EB1 by TIP60 ensures accurate spindle positioning in mitosis. <i>Nature Chemical Biology</i> , 2021, 17, 1314-1323.	3.9	29

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37	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.	1.8	28
38	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.	2.5	26
39	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.	1.8	26
40	Analysis of the Subcellular Phosphoproteome Using a Novel Phosphoproteomic Reactor. <i>Journal of Proteome Research</i> , 2010, 9, 1279-1288.	1.8	25
41	Evolution of Nucleic Acid Aptamers Capable of Specifically Targeting Glioma Stem Cells via Cell-SELEX. <i>Analytical Chemistry</i> , 2019, 91, 8070-8077.	3.2	25
42	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, 891-899.	1.3	24
43	An integrated strategy for highly sensitive phosphoproteome analysis from low micrograms of protein samples. <i>Analyst, The</i> , 2018, 143, 3693-3701.	1.7	24
44	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.	3.1	24
45	Spatial proteome profiling by immunohistochemistry-based laser capture microdissection and data-independent acquisition proteomics. <i>Analytica Chimica Acta</i> , 2020, 1127, 140-148.	2.6	23
46	Acetylation of ACAP4 regulates CCL18-elicited breast cancer cell migration and invasion. <i>Journal of Molecular Cell Biology</i> , 2018, 10, 559-572.	1.5	22
47	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.	1.8	21
48	Spatial proteomics for understanding the tissue microenvironment. <i>Analyst, The</i> , 2021, 146, 3777-3798.	1.7	21
49	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, 11023-11028.	3.3	19
50	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.	3.3	19
51	Dissecting the multi-omics atlas of the exosomes released by human lung adenocarcinoma stem-like cells. <i>Npj Genomic Medicine</i> , 2021, 6, 48.	1.7	18
52	Bruton's tyrosine kinase potentiates ALK signaling and serves as a potential therapeutic target of neuroblastoma. <i>Oncogene</i> , 2018, 37, 6180-6194.	2.6	17
53	Mass Spectrometry-Based Protein Complex Profiling in Time and Space. <i>Analytical Chemistry</i> , 2021, 93, 598-619.	3.2	17
54	Improvement of performance in label-free quantitative proteome analysis with monolithic electrospray ionization emitter. <i>Journal of Separation Science</i> , 2008, 31, 2589-2597.	1.3	16

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55	Analysis of low-abundance proteins using the proteomic reactor with pH fractionation. <i>Talanta</i> , 2010, 80, 1526-1531.	2.9	16
56	MST4 kinase phosphorylates ACAP4 protein to orchestrate apical membrane remodeling during gastric acid secretion. <i>Journal of Biological Chemistry</i> , 2017, 292, 16174-16187.	1.6	16
57	Fast quantitative urinary proteomic profiling workflow for biomarker discovery in kidney cancer. <i>Clinical Proteomics</i> , 2018, 15, 42.	1.1	16
58	Chemical proteomic study of isoprenoid chain interactome with a synthetic photoaffinity probe. <i>Proteomics</i> , 2008, 8, 3094-3104.	1.3	15
59	Integrated and Quantitative Proteomic Approach for Charting Temporal and Endogenous Protein Complexes. <i>Analytical Chemistry</i> , 2018, 90, 12574-12583.	3.2	15
60	Feedback control of PLK1 by Apolo1 ensures accurate chromosome segregation. <i>Cell Reports</i> , 2021, 36, 109343.	2.9	15
61	Biological fingerprinting analysis of the interactome of a kinase inhibitor in human plasma by a chemiproteomic approach. <i>Journal of Chromatography A</i> , 2006, 1134, 134-142.	1.8	14
62	Exploring intercellular signaling by proteomic approaches. <i>Proteomics</i> , 2014, 14, 498-512.	1.3	14
63	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.	3.2	14
64	Combinatory Data-Independent Acquisition and Parallel Reaction Monitoring Method for Deep Profiling of Gangliosides. <i>Analytical Chemistry</i> , 2020, 92, 10830-10838.	3.2	14
65	AutoProteome Chip System for Fully Automated and Integrated Proteomics Sample Preparation and Peptide Fractionation. <i>Analytical Chemistry</i> , 2020, 92, 8893-8900.	3.2	13
66	Phosphorylation of PP1 Regulator Sds22 by PLK1 Ensures Accurate Chromosome Segregation. <i>Journal of Biological Chemistry</i> , 2016, 291, 21123-21136.	1.6	12
67	OPA-Based Bifunctional Linker for Protein Labeling and Profiling. <i>Biochemistry</i> , 2020, 59, 175-178.	1.2	12
68	Facile synthesis of carboxymethyl- α -cyclodextrin conjugated magnetic nanoparticles for selective enrichment of glycopeptides. <i>Rapid Communications in Mass Spectrometry</i> , 2016, 30, 190-195.	0.7	11
69	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.	1.8	11
70	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.	0.7	11
71	Rapid and sensitive MRM-based mass spectrometry approach for systematically exploring ganglioside-protein interactions. <i>Proteomics</i> , 2013, 13, 1334-1338.	1.3	10
72	Time-of-Day- and Light-Dependent Expression of Ubiquitin Protein Ligase E3 Component N-Recognin 4 (UBR4) in the Suprachiasmatic Nucleus Circadian Clock. <i>PLoS ONE</i> , 2014, 9, e103103.	1.1	10

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73	CoreFlow: A computational platform for integration, analysis and modeling of complex biological data. <i>Journal of Proteomics</i> , 2014, 100, 167-173.	1.2	10
74	High-Throughput and Integrated Chemical Proteomic Approach for Profiling Phosphotyrosine Signaling Complexes. <i>Analytical Chemistry</i> , 2020, 92, 8933-8942.	3.2	10
75	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.	2.5	10
76	An enhanced chemically defined SILAC culture system for quantitative proteomics study of human embryonic stem cells. <i>Proteomics</i> , 2011, 11, 4040-4046.	1.3	9
77	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, 1007-1018.	1.1	9
78	Fully Integrated and Multiplexed Sample Preparation Technology for Sensitive Interactome Profiling. <i>Analytical Chemistry</i> , 2021, 93, 3026-3034.	3.2	9
79	Motif-dependent immune co-receptor interactome profiling by photoaffinity chemical proteomics. <i>Cell Chemical Biology</i> , 2022, 29, 1024-1036.e5.	2.5	8
80	Selective inhibition reveals the regulatory function of DYRK2 in protein synthesis and calcium entry. <i>ELife</i> , 2022, 11, .	2.8	8
81	High-Throughput Phosphotyrosine Protein Complexes Screening by Photoaffinity-Engineered Protein Scaffold-Based Forward-Phase Protein Array. <i>Analytical Chemistry</i> , 2019, 91, 10026-10032.	3.2	7
82	Combining Metabolic Alkyne Labeling and Click Chemistry for Secretome Analysis of ^αSerum-Containing ^βConditioned Medium. <i>Chinese Journal of Chemistry</i> , 2021, 39, 1843-1848.	2.6	7
83	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.	2.6	6
84	Fritted tip capillary column with negligible dead volume facilitated ultrasensitive and deep proteomics. <i>Analytica Chimica Acta</i> , 2022, 1201, 339615.	2.6	5
85	Proteomic Analysis of Secreted Proteins from Cell Microenvironment. <i>Methods in Molecular Biology</i> , 2017, 1662, 45-58.	0.4	4
86	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.	1.8	4
87	A fully integrated sample preparation strategy for highly sensitive intact glycoproteomics. <i>Analyst, The</i> , 2022, 147, 794-798.	1.7	4
88	SH2 Domains as Affinity Reagents for Phosphotyrosine Protein Enrichment and Proteomic Analysis. <i>Methods in Molecular Biology</i> , 2017, 1555, 395-406.	0.4	3
89	Multiomeric analysis of a dried single-drop plasma sample using an integrated mass spectrometry approach. <i>Analyst, The</i> , 2020, 145, 6441-6446.	1.7	3
90	Kindlin-2 promotes Src-mediated tyrosine phosphorylation of androgen receptor and contributes to breast cancer progression. <i>Cell Death and Disease</i> , 2022, 13, .	2.7	3

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91	Mass spectrometry-based ganglioside profiling provides potential insights into Alzheimer's disease development. <i>Journal of Chromatography A</i> , 2022, 1676, 463196.	1.8	3
92	Progress and Application of LC-MS Technologies for Characterizing Protein Post Translational Modifications. <i>Chinese Journal of Analytical Chemistry</i> , 2015, 43, 1479-1489.	0.9	2
93	Generic Plug-and-Play Strategy for High-Throughput Analysis of PTM-Mediated Protein Complexes. <i>Analytical Chemistry</i> , 2022, 94, 6799-6808.	3.2	1
94	Fe ³⁺ O ⁴⁻ /ethylenediaminetetraacetic acid magnetic beads-based integrated method for proteomic analysis. <i>Chinese Journal of Chromatography (Se Pu)</i> , 2016, 34, 1264.	0.1	0
95	Zwitter-ionic Monolith-based Spintip Column Coupled with Evosep One Liquid Chromatography for High-throughput Proteomic Analysis. <i>Journal of Chromatography A</i> , 2022, , 463122.	1.8	0