

Yichu Shan

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

1,501
citations

279701

23
h-index

345118

36
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66
all docs

66
docs citations

66
times ranked

2017
citing authors

#	ARTICLE	IF	CITATIONS
1	Effective isolation of exosomes with polyethylene glycol from cell culture supernatant for in-depth proteome profiling. <i>Analyst</i> , The, 2016, 141, 4640-4646.	1.7	187
2	Human Metapneumovirus Glycoprotein G Inhibits Innate Immune Responses. <i>PLoS Pathogens</i> , 2008, 4, e1000077.	2.1	104
3	Immobilized enzyme reactors in proteomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2011, 30, 691-702.	5.8	82
4	Determination of peptides and amino acids from wool and beer with sensitive fluorescent reagent 2-(9-carbazole)-ethyl chloroformate by reverse phase high-performance liquid chromatography and liquid chromatography mass spectrometry. <i>Analytical Biochemistry</i> , 2003, 313, 17-27.	1.1	64
5	Human Metapneumovirus Small Hydrophobic Protein Inhibits NF- κ B Transcriptional Activity. <i>Journal of Virology</i> , 2008, 82, 8224-8229.	1.5	55
6	Organic-Inorganic Hybrid Silica Monolith Based Immobilized Titanium Ion Affinity Chromatography Column for Analysis of Mitochondrial Phosphoproteome. <i>Journal of Proteome Research</i> , 2010, 9, 4093-4101.	1.8	53
7	Hydrophobic Tagging-Assisted N-Termini Enrichment for In-Depth N-Terminome Analysis. <i>Analytical Chemistry</i> , 2016, 88, 8390-8395.	3.2	50
8	Application of probabilistic neural network in the clinical diagnosis of cancers based on clinical chemistry data. <i>Analytica Chimica Acta</i> , 2002, 471, 77-86.	2.6	40
9	Mass Defect-Based Pseudo-Isobaric Dimethyl Labeling for Proteome Quantification. <i>Analytical Chemistry</i> , 2013, 85, 10658-10663.	3.2	40
10	Recent advances in stable isotope labeling based techniques for proteome relative quantification. <i>Journal of Chromatography A</i> , 2014, 1365, 1-11.	1.8	38
11	Recent advances in micro-scale and nano-scale high-performance liquid-phase chromatography for proteome research. <i>Analytical and Bioanalytical Chemistry</i> , 2011, 399, 229-241.	1.9	37
12	Integrated Device for Online Sample Buffer Exchange, Protein Enrichment, and Digestion. <i>Analytical Chemistry</i> , 2010, 82, 2574-2579.	3.2	36
13	Mn (III) tetrakis (4-benzoic acid) porphyrin scavenges reactive species, reduces oxidative stress, and improves functional recovery after experimental spinal cord injury in rats: comparison with methylprednisolone. <i>BMC Neuroscience</i> , 2013, 14, 23.	0.8	36
14	Integration of capillary isoelectric focusing with monolithic immobilized pH gradient, immobilized trypsin microreactor and capillary zone electrophoresis for on-line protein analysis. <i>Journal of Separation Science</i> , 2010, 33, 3194-3200.	1.3	35
15	In-Depth Proteomic Quantification of Cell Secretome in Serum-Containing Conditioned Medium. <i>Analytical Chemistry</i> , 2016, 88, 4971-4978.	3.2	35
16	Breakthrough curves and elution profiles of single solutes in case of adsorption isotherms with two inflection points. <i>Journal of Chromatography A</i> , 2006, 1107, 216-225.	1.8	34
17	Coupling Formic Acid Assisted Solubilization and Online Immobilized Pepsin Digestion with Strong Cation Exchange and Microflow Reversed-Phase Liquid Chromatography with Electrospray Ionization Tandem Mass Spectrometry for Integral Membrane Proteome Analysis. <i>Analytical Chemistry</i> , 2010, 82, 9622-9625.	3.2	33
18	Optimization of gradient elution conditions in multicomponent preparative liquid chromatography. <i>Journal of Chromatography A</i> , 2005, 1093, 47-58.	1.8	31

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19	Ionic liquid 1-butyl-3-methyl imidazolium tetrafluoroborate for shotgun membrane proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2011, 399, 3387-3397.	1.9	30
20	Analysis of the isolation of a target component using multicomponent isocratic preparative elution chromatography. <i>Journal of Chromatography A</i> , 2004, 1041, 53-62.	1.8	27
21	Surface modification with highly-homogeneous porous silica layer for enzyme immobilization in capillary enzyme microreactors. <i>Talanta</i> , 2019, 197, 539-547.	2.9	27
22	Micronutrient Requirements for Growth and Hydrocarbon Production in the Oil Producing Green Alga <i>Botryococcus braunii</i> (Chlorophyta). <i>PLoS ONE</i> , 2012, 7, e41459.	1.1	27
23	In-Depth Proteome Coverage by Improving Efficiency for Membrane Proteome Analysis. <i>Analytical Chemistry</i> , 2017, 89, 5179-5185.	3.2	26
24	Multi-omics analysis to reveal disorders of cell metabolism and integrin signaling pathways induced by PM2.5. <i>Journal of Hazardous Materials</i> , 2022, 424, 127573.	6.5	25
25	Monodisperse Boronate Polymeric Particles Synthesized by a Precipitation Polymerization Strategy: Particle Formation and Glycoprotein Response from the Standpoint of the Flory-Huggins Model. <i>ACS Applied Materials & Interfaces</i> , 2014, 6, 2059-2066.	4.0	24
26	Releasing N-glycan from Peptide N-terminus by N-terminal Succinylation Assisted Enzymatic Deglycosylation. <i>Scientific Reports</i> , 2015, 5, 9770.	1.6	19
27	Development of a Highly Efficient 2-D System with a Serially Coupled Long Column and Its Application in Identification of Rat Brain Integral Membrane Proteins with Ionic Liquids-Assisted Solubilization and Digestion. <i>Journal of Proteome Research</i> , 2011, 10, 732-738.	1.8	18
28	Protein separation using free-flow electrophoresis microchip etched in a single step. <i>Journal of Separation Science</i> , 2010, 33, 2039-2044.	1.3	17
29	Monoliths with immobilized zirconium ions for selective enrichment of phosphopeptides. <i>Journal of Separation Science</i> , 2011, 34, 2113-2121.	1.3	17
30	Octyl-functionalized hybrid magnetic mesoporous microspheres for enrichment of low-concentration peptides prior to direct analysis by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2011, 25, 1257-1265.	0.7	16
31	Integration of normal phase liquid chromatography with supercritical fluid chromatography for analysis of fruiting bodies of <i>Ganoderma lucidum</i> . <i>Journal of Separation Science</i> , 2010, 33, 3817-3821.	1.3	15
32	HPLC-MS/MS shotgun proteomic research of deer antlers with multiparallel protein extraction methods. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2010, 878, 3370-3374.	1.2	14
33	A Multiplex Fragment-Ion-Based Method for Accurate Proteome Quantification. <i>Analytical Chemistry</i> , 2019, 91, 3921-3928.	3.2	13
34	Preparative separation of major xanthenes from mangosteen pericarp using high-performance centrifugal partition chromatography. <i>Journal of Separation Science</i> , 2010, 33, 1274-1278.	1.3	12
35	A paired ions scoring algorithm based on Morpheus for simultaneous identification and quantification of proteome samples prepared by isobaric peptide termini labeling strategies. <i>Proteomics</i> , 2015, 15, 1781-1788.	1.3	12
36	Ionic liquid-based method for direct proteome characterization of velvet antler cartilage. <i>Talanta</i> , 2016, 161, 541-546.	2.9	12

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37	Pseudo isobaric peptide termini labelling for relative proteome quantification by SWATH MS acquisition. <i>Analyst, The</i> , 2016, 141, 4912-4918.	1.7	12
38	Depletion of internal peptides by site-selective blocking, phosphate labeling, and TiO ₂ adsorption for in-depth analysis of C-terminome. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 3867-3874.	1.9	11
39	Site-Specific Quantification of Persulfidome by Combining an Isotope-Coded Affinity Tag with Strong Cation-Exchange-Based Fractionation. <i>Analytical Chemistry</i> , 2019, 91, 14860-14864.	3.2	11
40	Comprehensive Analysis of Protein N-Terminome by Guanidination of Terminal Amines. <i>Analytical Chemistry</i> , 2020, 92, 567-572.	3.2	11
41	Carboxypeptidase B-Assisted Charge-Based Fractional Diagonal Chromatography for Deep Screening of C-Terminome. <i>Analytical Chemistry</i> , 2020, 92, 8005-8009.	3.2	10
42	Fast MS/MS acquisition without dynamic exclusion enables precise and accurate quantification of proteome by MS/MS fragment intensity. <i>Scientific Reports</i> , 2016, 6, 26392.	1.6	9
43	Advances and applications of stable isotope labeling-based methods for proteome relative quantitation. <i>TrAC - Trends in Analytical Chemistry</i> , 2020, 124, 115815.	5.8	9
44	Stability, Disposition, and Penetration of Catalytic Antioxidants Mn-Porphyrin and Mn-Salen and of Methylprednisolone in Spinal Cord Injury. <i>Central Nervous System Agents in Medicinal Chemistry</i> , 2012, 12, 122-130.	0.5	9
45	Glycoprotein recognition by water-compatible core-shell polymeric submicron particles. <i>Journal of Materials Chemistry B</i> , 2015, 3, 3927-3930.	2.9	8
46	Partially isobaric peptide termini labeling assisted proteome quantitation based on MS and MS/MS signals. <i>Journal of Proteomics</i> , 2015, 114, 152-160.	1.2	8
47	Multi-segment linear gradient optimization strategy based on resolution map in HPLC. <i>Science in China Series B: Chemistry</i> , 2006, 49, 315-325.	0.8	7
48	Smart Cutter: An Efficient Strategy for Increasing the Coverage of Chemical Cross-Linking Analysis. <i>Analytical Chemistry</i> , 2020, 92, 1097-1105.	3.2	6
49	RETENTION MODELING AND OPTIMIZATION OF pH VALUE AND SOLVENT COMPOSITION IN HPLC USING BACK-PROPAGATION NEURAL NETWORKS AND UNIFORM DESIGN. <i>Journal of Liquid Chromatography and Related Technologies</i> , 2002, 25, 1033-1047.	0.5	5
50	Retention modeling and simultaneous optimization of pH value and gradient steepness in RP-HPLC using feed-forward neural networks. <i>Journal of Separation Science</i> , 2003, 26, 1541-1546.	1.3	5
51	High sensitive protein detection by hollow fiber membrane interface based protein enrichment and in situ fluorescence derivatization. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2011, 879, 1439-1443.	1.2	5
52	A1 Ions: Peptide-Specific and Intensity-Enhanced Fragment Ions for Accurate and Multiplexed Proteome Quantitation. <i>Analytical Chemistry</i> , 2022, 94, 7637-7646.	3.2	5
53	Weak anion and cation exchange mixed-bed microcolumn for protein separation. <i>Journal of Separation Science</i> , 2010, 33, 3299-3303.	1.3	4
54	Improved accuracy for label-free absolute quantification of proteome by combining the absolute protein expression profiling algorithm and summed tandem mass spectrometric total ion current. <i>Analyst, The</i> , 2014, 139, 138-146.	1.7	4

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55	Label-free quantification of differentially expressed proteins in mouse liver cancer cells with high and low metastasis rates by a SWATH acquisition method. <i>Science China Chemistry</i> , 2014, 57, 718-722.	4.2	4
56	Antibody-free enrichment method for proteome-wide analysis of endogenous SUMOylation sites. <i>Analytica Chimica Acta</i> , 2021, 1154, 338324.	2.6	4
57	All-Ion Monitoring-Directed Low-Abundance Protein Quantification Reveals CALB2 as a Key Promoter in Hepatocellular Carcinoma Metastasis. <i>Analytical Chemistry</i> , 2022, , .	3.2	4
58	Combination of continuous digestion by peptidase and spectral similarity comparisons for peptide sequencing. <i>Journal of Separation Science</i> , 2020, 43, 3665-3673.	1.3	2
59	Sequential amidation of peptide C-termini for improving fragmentation efficiency. <i>Journal of Mass Spectrometry</i> , 2021, 56, e4529.	0.7	2
60	NIPTL-Novo: Non-isobaric peptide termini labeling assisted peptide de novo sequencing. <i>Journal of Proteomics</i> , 2017, 154, 40-48.	1.2	1
61	Improved Accuracy of Proteome Quantification by MS/MS Fragment Intensity. <i>FASEB Journal</i> , 2015, 29, 567.9.	0.2	0