

Xinning Jiang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/676739/publications.pdf>

Version: 2024-02-01

34
papers

2,255
citations

331670

21
h-index

377865

34
g-index

34
all docs

34
docs citations

34
times ranked

3211
citing authors

#	ARTICLE	IF	CITATIONS
1	Glycoproteomics Analysis of Human Liver Tissue by Combination of Multiple Enzyme Digestion and Hydrazide Chemistry. <i>Journal of Proteome Research</i> , 2009, 8, 651-661.	3.7	356
2	Specific Phosphopeptide Enrichment with Immobilized Titanium Ion Affinity Chromatography Adsorbent for Phosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2008, 7, 3957-3967.	3.7	239
3	Immobilized Zirconium Ion Affinity Chromatography for Specific Enrichment of Phosphopeptides in Phosphoproteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1656-1665.	3.8	228
4	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.	2.2	192
5	Systematic Analysis of Protein Phosphorylation Networks From Phosphoproteomic Data. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1070-1083.	3.8	161
6	Reversed-Phase-Reversed-Phase Liquid Chromatography Approach with High Orthogonality for Multidimensional Separation of Phosphopeptides. <i>Analytical Chemistry</i> , 2010, 82, 53-56.	6.5	135
7	Method Development of Efficient Protein Extraction in Bone Tissue for Proteome Analysis. <i>Journal of Proteome Research</i> , 2007, 6, 2287-2294.	3.7	128
8	Preparation of monodisperse immobilized Ti ⁴⁺ affinity chromatography microspheres for specific enrichment of phosphopeptides. <i>Analytica Chimica Acta</i> , 2009, 636, 34-41.	5.4	105
9	Development of Efficient Protein Extraction Methods for Shotgun Proteome Analysis of Formalin-Fixed Tissues. <i>Journal of Proteome Research</i> , 2007, 6, 1038-1047.	3.7	92
10	Comparative proteomic analysis of <i>Rhodosporidium toruloides</i> during lipid accumulation. <i>Yeast</i> , 2009, 26, 553-566.	1.7	72
11	Phosphoproteome analysis of human liver tissue by long gradient nanoflow LC coupled with multiple stage MS analysis. <i>Electrophoresis</i> , 2010, 31, 1080-1089.	2.4	61
12	Perspectives of Comprehensive Phosphoproteome Analysis Using Shotgun Strategy. <i>Analytical Chemistry</i> , 2011, 83, 8078-8085.	6.5	50
13	The proteome analysis of oleaginous yeast <i>Lipomyces starkeyi</i> . <i>FEMS Yeast Research</i> , 2011, 11, 42-51.	2.3	43
14	Comprehensive Peptidome Analysis of Mouse Livers by Size Exclusion Chromatography Prefractionation and NanoLC-MS/MS Identification. <i>Journal of Proteome Research</i> , 2007, 6, 801-808.	3.7	42
15	Automatic Validation of Phosphopeptide Identifications by the MS ₂ /MS ₃ Target-Decoy Search Strategy. <i>Journal of Proteome Research</i> , 2008, 7, 1640-1649.	3.7	40
16	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.	2.2	38
17	Proteome-Wide Discovery and Characterizations of Nucleotide-Binding Proteins with Affinity-Labeled Chemical Probes. <i>Analytical Chemistry</i> , 2013, 85, 3198-3206.	6.5	27
18	Comprehensive and Reliable Phosphorylation Site Mapping of Individual Phosphoproteins by Combination of Multiple Stage Mass Spectrometric Analysis with a Target-Decoy Database Search. <i>Analytical Chemistry</i> , 2009, 81, 5794-5805.	6.5	25

#	ARTICLE	IF	CITATIONS
19	Optimization of filtering criterion for SEQUEST database searching to improve proteome coverage in shotgun proteomics. <i>BMC Bioinformatics</i> , 2007, 8, 323.	2.6	24
20	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.	3.7	21
21	ArMone: A Software Suite Specially Designed for Processing and Analysis of Phosphoproteome Data. <i>Journal of Proteome Research</i> , 2010, 9, 2743-2751.	3.7	21
22	Spatial Phosphoprotein Profiling Reveals a Compartmentalized Extracellular Signal-regulated Kinase Switch Governing Neurite Growth and Retraction. <i>Journal of Biological Chemistry</i> , 2011, 286, 18190-18201.	3.4	19
23	Improvement of performance in label-free quantitative proteome analysis with monolithic electrospray ionization emitter. <i>Journal of Separation Science</i> , 2008, 31, 2589-2597.	2.5	16
24	Fractionation of phosphopeptides on strong anion-exchange capillary trap column for large-scale phosphoproteome analysis of microgram samples. <i>Journal of Separation Science</i> , 2010, 33, 1879-1887.	2.5	16
25	Global Proteome Quantification for Discovering Imatinib-Induced Perturbation of Multiple Biological Pathways in K562 Human Chronic Myeloid Leukemia Cells. <i>Journal of Proteome Research</i> , 2010, 9, 6007-6015.	3.7	15
26	Classification Filtering Strategy to Improve the Coverage and Sensitivity of Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2010, 82, 6168-6175.	6.5	15
27	Quantitative Proteomic Analysis Reveals the Perturbation of Multiple Cellular Pathways in Jurkat-T Cells Induced by Doxorubicin. <i>Journal of Proteome Research</i> , 2010, 9, 5943-5951.	3.7	15
28	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.	3.7	14
29	Quantitative Proteomic Analysis Revealed Lovastatin-induced Perturbation of Cellular Pathways in HL-60 Cells. <i>Journal of Proteome Research</i> , 2011, 10, 5463-5471.	3.7	14
30	Identification of Angiotensin Converting Enzyme Inhibitors in Peptides Mixture of Hydrolyzed Red Deer Plasma with Proteomic Approach. <i>Chinese Journal of Chemistry</i> , 2010, 28, 1665-1672.	4.9	13
31	Procedures for the biochemical enrichment and proteomic analysis of the cytoskeleton. <i>Analytical Biochemistry</i> , 2014, 446, 102-107.	2.4	10
32	Proteomic and Biochemical Methods to Study the Cytoskeleton. <i>Methods in Molecular Biology</i> , 2013, 1046, 203-218.	0.9	5
33	Instance Based Algorithm for Posterior Probability Calculation by Target-Decoy Strategy to Improve Protein Identifications. <i>Analytical Chemistry</i> , 2008, 80, 9326-9335.	6.5	2
34	Enrichment of peptides containing consensus sequence by an enzymatic approach for targeted analysis of proteins. <i>Proteomics</i> , 2011, 11, 3578-3581.	2.2	1