

Jie Dai

List of Publications by Year in descending order

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27
papers

1,234
citations

361413
20
h-index

526287
27
g-index

27
all docs

27
docs citations

27
times ranked

1944
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomic analysis reveals wide distribution of phototrophic bacteria in hydrothermal vents on the ultraslow-spreading Southwest Indian Ridge. <i>Marine Life Science and Technology</i> , 2022, 4, 255-267.	4.6	4
2	Resazurin as an indicator of reducing capacity for analyzing the physiologic status of deep-sea bacterium <i>Photobacterium phosphoreum</i> ANT-2200. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 297-305.	1.3	5
3	<i>Crassaminicella thermophila</i> sp. nov., a moderately thermophilic bacterium isolated from a deep-sea hydrothermal vent chimney and emended description of the genus <i>Crassaminicella</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	12
4	Nuclear phosphoproteome analysis of 3T3L1 preadipocyte differentiation reveals system-wide phosphorylation of transcriptional regulators. <i>Proteomics</i> , 2017, 17, 1600248.	2.2	10
5	Revealing the functional structure of a new PLA2 K49 from <i>Bothriopsis taeniata</i> snake venom employing automatic de novo sequencing using CID/HCD/ETD MS/MS analyses. <i>Journal of Proteomics</i> , 2016, 131, 131-139.	2.4	7
6	Preprocessing Significantly Improves the Peptide/Protein Identification Sensitivity of High-resolution Isobarically Labeled Tandem Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 405-417.	3.8	27
7	The Cultural Divide: Exponential Growth in Classical 2D and Metabolic Equilibrium in 3D Environments. <i>PLoS ONE</i> , 2014, 9, e106973.	2.5	52
8	Quantitative phosphoproteomic analysis of porcine muscle within 24 h postmortem. <i>Journal of Proteomics</i> , 2014, 106, 125-139.	2.4	49
9	Quantitative Proteomics Reveal up-regulated Protein Expression of the SET Complex Associated with Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2012, 11, 871-885.	3.7	30
10	BuildSummary: Using a Group-Based Approach To Improve the Sensitivity of Peptide/Protein Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 1494-1502.	3.7	52
11	Large Scale Phosphoproteome Profiles Comprehensive Features of Mouse Embryonic Stem Cells. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.001750.	3.8	29
12	A comprehensive and non-prefractionation on the protein level approach for the human urinary proteome: touching phosphorylation in urine. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 823-832.	1.5	79
13	High-coverage proteome analysis reveals the first insight of protein modification systems in the pathogenic spirochete <i>Leptospira interrogans</i> . <i>Cell Research</i> , 2010, 20, 197-210.	12.0	60
14	Proteome, Phosphoproteome, and Hydroxyproteome of Liver Mitochondria in Diabetic Rats at Early Pathogenic Stages. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 100-116.	3.8	100
15	Comprehensive Profiling of Phosphopeptides Based on Anion Exchange Followed by Flow-Through Enrichment with Titanium Dioxide (AFET). <i>Journal of Proteome Research</i> , 2010, 9, 4585-4594.	3.7	37
16	Concurrent Quantification of Proteome and Phosphoproteome to Reveal System-wide Association of Protein Phosphorylation and Gene Expression. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2809-2826.	3.8	34
17	Temporal and spatial profiling of nuclei-associated proteins upon TNF- α /NF- κ B signaling. <i>Cell Research</i> , 2009, 19, 651-664.	12.0	20
18	Fully Automatic Separation and Identification of Phosphopeptides by Continuous pH-Gradient Anion Exchange Online Coupled with Reversed-Phase Liquid Chromatography Mass Spectrometry. <i>Journal of Proteome Research</i> , 2009, 8, 133-141.	3.7	59

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19	Fractionation of Complex Protein Mixture by Virtual Three-Dimensional Liquid Chromatography Based on Combined pH and Salt Steps. <i>Journal of Proteome Research</i> , 2008, 7, 4525-4537.	3.7	20
20	Localized-Statistical Quantification of Human Serum Proteome Associated with Type 2 Diabetes. <i>PLoS ONE</i> , 2008, 3, e3224.	2.5	67
21	Quantitative Phosphoproteome Profiling of Wnt3a-mediated Signaling Network. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1952-1967.	3.8	57
22	Protein Phosphorylation and Expression Profiling by Yin-Yang Multidimensional Liquid Chromatography (Yin-Yang MDLC) Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 250-262.	3.7	123
23	A fully automated LC-MS method utilizing online continuous pH and RP gradients for global proteome analysis. <i>Electrophoresis</i> , 2007, 28, 4311-4319.	2.4	47
24	The human plasma proteome: Analysis of Chinese serum using shotgun strategy. <i>Proteomics</i> , 2005, 5, 3442-3453.	2.2	66
25	Proteomic Analysis with Integrated Multiple Dimensional Liquid Chromatography/Mass Spectrometry Based on Elution of Ion Exchange Column Using pH Steps. <i>Analytical Chemistry</i> , 2005, 77, 5793-5799.	6.5	75
26	Human Plasma Proteome Analysis by Multidimensional Chromatography Prefractionation and Linear Ion Trap Mass Spectrometry Identification. <i>Journal of Proteome Research</i> , 2005, 4, 613-619.	3.7	74
27	High-Sensitivity Analysis of Human Plasma Proteome by Immobilized Isoelectric Focusing Fractionation Coupled to Mass Spectrometry Identification. <i>Journal of Proteome Research</i> , 2005, 4, 1265-1273.	3.7	39