

Shenheng Guan

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

832
citations

567281

15
h-index

752698

20
g-index

21
all docs

21
docs citations

21
times ranked

1494
citing authors

#	ARTICLE	IF	CITATIONS
1	Data Dependentâ€“Independent Acquisition (DDIA) Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 3230-3237.	3.7	39
2	Repeat-Preserving Decoy Database for False Discovery Rate Estimation in Peptide Identification. <i>Journal of Proteome Research</i> , 2020, 19, 1029-1036.	3.7	24
3	Prediction of LC-MS/MS Properties of Peptides from Sequence by Deep Learning. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2099-2107.	3.8	43
4	Spindlinâ€“1 recognizes methylations of K20 and R23 of histone H4 tail. <i>FEBS Letters</i> , 2018, 592, 4098-4110.	2.8	12
5	Evidence for sortilin modulating regional accumulation of human tau prions in transgenic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E11029-E11036.	7.1	23
6	Characterization of Dynamic UbR-Proteasome Subcomplexes by In vivo Cross-linking (X) Assisted Bimolecular Tandem Affinity Purification (XBAP) and Label-free Quantitation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2279-2292.	3.8	33
7	Optimization of Aryl Amides that Extend Survival in Prion-Infected Mice. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2016, 358, 537-547.	2.5	27
8	Oligomerization between BSU1 Family Members Potentiates Brassinosteroid Signaling in Arabidopsis. <i>Molecular Plant</i> , 2016, 9, 178-181.	8.3	27
9	Deconvolution Method for Specific and Nonspecific Binding of Ligand to Multiprotein Complex by Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 8541-8546.	6.5	15
10	Different 2-Aminothiazole Therapeutics Produce Distinct Patterns of Scrapie Prion Neuropathology in Mouse Brains. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2015, 355, 2-12.	2.5	43
11	Improved Peak Detection and Deconvolution of Native Electrospray Mass Spectra from Large Protein Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 2141-2151.	2.8	49
12	A New in Vivo Cross-linking Mass Spectrometry Platform to Define Proteinâ€“Protein Interactions in Living Cells. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3533-3543.	3.8	167
13	Compartment Modeling for Mammalian Protein Turnover Studies by Stable Isotope Metabolic Labeling. <i>Analytical Chemistry</i> , 2012, 84, 4014-4021.	6.5	64
14	A Data Processing Pipeline for Mammalian Proteome Dynamics Studies Using Stable Isotope Metabolic Labeling. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010728.	3.8	124
15	High mass selectivity for top-down proteomics by application of SWIFT technology. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 455-459.	2.8	15
16	Data Processing Algorithms for Analysis of High Resolution MSMS Spectra of Peptides with Complex Patterns of Posttranslational Modifications. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 804-810.	3.8	39
17	Using Mass Spectrometry to Characterize the Complex Posttranslational Modifications of Histones. <i>FASEB Journal</i> , 2006, 20, A100.	0.5	0
18	Generation of optimal excitation pulses for two energy level systems using an inverse Fourier transform method. <i>Journal of Chemical Physics</i> , 1992, 96, 7959-7964.	3.0	13

#	ARTICLE	IF	CITATIONS
19	Linear response theory of ion excitation for Fourier transform mass spectrometry. Journal of the American Society for Mass Spectrometry, 1991, 2, 483-486.	2.8	30
20	Optimal phase modulation in stored waveform inverse Fourier transform excitation for Fourier transform mass spectrometry. II. Magnitude spectrum smoothing. Journal of Chemical Physics, 1990, 93, 8442-8445.	3.0	13
21	Optimal phase modulation in stored wave form inverse Fourier transform excitation for Fourier transform mass spectrometry. I. Basic algorithm. Journal of Chemical Physics, 1990, 92, 5841-5846.	3.0	32