

Qin Fu

List of Publications by Year in descending order

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14
papers

706
citations

933447

10
h-index

1125743

13
g-index

16
all docs

16
docs citations

16
times ranked

1293
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated proteomic sample preparation: The key component for high throughput and quantitative mass spectrometry analysis. <i>Mass Spectrometry Reviews</i> , 2023, 42, 873-886.	5.4	11
2	Standardized Workflow for Precise Mid- and High-Throughput Proteomics of Blood Biofluids. <i>Clinical Chemistry</i> , 2022, 68, 450-460.	3.2	22
3	A Dual Workflow to Improve the Proteomic Coverage in Plasma Using Data-Independent Acquisition-MS. <i>Journal of Proteome Research</i> , 2020, 19, 2828-2837.	3.7	11
4	Identification of Putative Early Atherosclerosis Biomarkers by Unsupervised Deconvolution of Heterogeneous Vascular Proteomes. <i>Journal of Proteome Research</i> , 2020, 19, 2794-2806.	3.7	16
5	A Plasma Sample Preparation for Mass Spectrometry using an Automated Workstation. <i>Journal of Visualized Experiments</i> , 2020, , .	0.3	15
6	A protocol integrating remote patient monitoring patient reported outcomes and cardiovascular biomarkers. <i>Npj Digital Medicine</i> , 2019, 2, 84.	10.9	12
7	Highly Reproducible Automated Proteomics Sample Preparation Workflow for Quantitative Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 420-428.	3.7	68
8	Sex differences in ischemic heart disease and heart failure biomarkers. <i>Biology of Sex Differences</i> , 2018, 9, 43.	4.1	35
9	An Empirical Approach to Signature Peptide Choice for Selected Reaction Monitoring: Quantification of Uromodulin in Urine. <i>Clinical Chemistry</i> , 2016, 62, 198-207.	3.2	19
10	Multiple and Selective Reaction Monitoring Using Triple Quadrupole Mass Spectrometer: Preclinical Large Cohort Analysis. <i>Methods in Molecular Biology</i> , 2016, 1410, 249-264.	0.9	16
11	Comparison of Multiplex Immunoassay Platforms. <i>Clinical Chemistry</i> , 2010, 56, 314-318.	3.2	189
12	A Rapid, Economical, and Reproducible Method for Human Serum Delipidation and Albumin and IgG Removal for Proteomic Analysis. , 2007, 357, 365-372.		21
13	Investigation of an albumin-enriched fraction of human serum and its albuminome. <i>Proteomics - Clinical Applications</i> , 2007, 1, 73-88.	1.6	165
14	A robust, streamlined, and reproducible method for proteomic analysis of serum by delipidation, albumin and IgG depletion, and two-dimensional gel electrophoresis. <i>Proteomics</i> , 2005, 5, 2656-2664.	2.2	104