Chen Shao

List of Publications by Year
in descending order

29 papers	736 citations	623734 14 h-index	610901 24 g-index
31 all docs	31 docs citations	31 times ranked	1303 citing authors

#	ARTICLE	IF	CITATIONS
1	A comprehensive analysis and annotation of human normal urinary proteome. Scientific Reports, 2017, 7, 3024.	3.3	127
2	A Tool for Biomarker Discovery in the Urinary Proteome: A Manually Curated Human and Animal Urine Protein Biomarker Database. Molecular and Cellular Proteomics, 2011, 10, M111.010975.	3.8	85
3	An Attempt to Understand Kidney's Protein Handling Function by Comparing Plasma and Urine Proteomes. PLoS ONE, 2009, 4, e5146.	2.5	60
4	A comprehensive map and functional annotation of the normal human cerebrospinal fluid proteome. Journal of Proteomics, 2015, 119, 90-99.	2.4	57
5	A Comparative Proteomics Analysis of Five Body Fluids: Plasma, Urine, Cerebrospinal Fluid, Amniotic Fluid, and Saliva. Proteomics - Clinical Applications, 2018, 12, e1800008.	1.6	53
6	A Proteomic Analysis of Individual and Gender Variations in Normal Human Urine and Cerebrospinal Fluid Using iTRAQ Quantification. PLoS ONE, 2015, 10, e0133270.	2.5	52
7	Comprehensive Analysis of Individual Variation in the Urinary Proteome Revealed Significant Gender Differences. Molecular and Cellular Proteomics, 2019, 18, 1110-1122.	3.8	50
8	Dynamic changes of urinary proteins in a focal segmental glomerulosclerosis rat model. Proteome Science, 2014, 12, 42.	1.7	39
9	Applications of urinary proteomics in biomarker discovery. Science China Life Sciences, 2011, 54, 409-417.	4.9	33
10	Differential ConA-enriched urinary proteome in rat experimental glomerular diseases. Biochemical and Biophysical Research Communications, 2008, 371, 385-390.	2.1	31
11	Differential urinary glycoproteome analysis of type 2 diabetic nephropathy using 2D-LC–MS/MS and iTRAQ quantification. Journal of Translational Medicine, 2015, 13, 371.	4.4	29
12	An individual urinary proteome analysis in normal human beings to define the minimal sample number to represent the normal urinary proteome. Proteome Science, 2012, 10, 70.	1.7	27
13	A dynamic mouse peptidome landscape reveals probiotic modulation of the gut-brain axis. Science Signaling, 2020, 13, .	3.6	17
14	Statistical characterization of HCD fragmentation patterns of tryptic peptides on an LTQ Orbitrap Velos mass spectrometer. Journal of Proteomics, 2014, 109, 26-37.	2.4	15
15	Urinary Protein Biomarker Database: A Useful Tool for Biomarker Discovery. Advances in Experimental Medicine and Biology, 2015, 845, 195-203.	1.6	12
16	Oscore: a combined score to reduce false negative rates for peptide identification in tandem mass spectrometry analysis. Journal of Mass Spectrometry, 2009, 44, 25-31.	1.6	11
17	Data for a comprehensive map and functional annotation of the human cerebrospinal fluid proteome. Data in Brief, 2015, 3, 103-107.	1.0	11
18	Improving peptide identification using an empirical peptide retention time database. Rapid Communications in Mass Spectrometry, 2009, 23, 109-118.	1.5	7

#	ARTICLE	IF	CITATIONS
19	Urinary Proteomic Characteristics of Hyperuricemia and Their Possible Links with the Occurrence of Its Concomitant Diseases. ACS Omega, 2021, 6, 9500-9508.	3.5	6
20	Differential urinary proteomics analysis of myocardial infarction using iTRAQ quantification. Molecular Medicine Reports, 2019, 19, 3972-3988.	2.4	5
21	A qualitative and quantitative analysis of the human gingival crevicular fluid proteome and metaproteome. Proteomics, 2021, 21, e2000321.	2.2	5
22	Applications of Peptide Retention Time in Proteomic Data Analysis. Advances in Experimental Medicine and Biology, 2015, 845, 67-75.	1.6	2
23	systematic analysis of a simple adaptor protein PDZK1: ligand identification, interaction and functional prediction of complex. FASEB Journal, 2009, 23, 516.1.	0.5	1
24	An Efficiency machine learning system prediction coupled with yeast two hybrid confirmations to identify HPV 16 E6 interacting PDZ proteins. FASEB Journal, 2009, 23, 858.9.	0.5	1
25	An integrated machine learning system to computationally screen protein databases for Protein binding peptide ligands.. FASEB Journal, 2006, 20, A528.	0.5	0
26	Understanding kidney function by comparing serum and urine proteomes. FASEB Journal, 2007, 21, A1004.	0.5	0
27	Improve the tandem mass spectra identification and reduce false negative rate using peptide LC retention time.. FASEB Journal, 2007, 21, A265.	0.5	0
28	The urinary biomarker database. FASEB Journal, 2011, 25, .	0.5	0
29	Comparison at the peptide level with post-translational modification consideration reveals more differences between two unenriched samples (778.1). FASEB Journal, 2014, 28, 778.1.	0.5	0