Zhengguang Guo

List of Publications by Year
in descending order

52 papers	959 citations	471509 17 h-index	501196 28 g-index
54 all docs	54 docs citations	54 times ranked	1783 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 comprehensive map and functional annotation of the normal human cerebrospinal fluid proteome. Journal of Proteomics, 2015, 119, 90-99.	2.4	57
3	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
4	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
5	Comprehensive Analysis of Individual Variation in the Urinary Proteome Revealed Significant Gender Differences. Molecular and Cellular Proteomics, 2019, 18, 1110-1122.	3.8	50
6	Dynamic changes of urine proteome in a Walker 256 tumor†bearing rat model. Cancer Medicine, 2017, 6, 2713-2722.	2.8	48
7	A novel TP53 pathway influences the HGS-mediated exosome formation in colorectal cancer. Scientific Reports, 2016, 6, 28083.	3.3	45
8	Metabolomics of Non-muscle Invasive Bladder Cancer: Biomarkers for Early Detection of Bladder Cancer. Frontiers in Oncology, 2018, 8, 494.	2.8	43
9	Urine Metabolomics for Renal Cell Carcinoma (RCC) Prediction: Tryptophan Metabolism as an Important Pathway in RCC. Frontiers in Oncology, 2019, 9, 663.	2.8	32
10	LC-MS-Based Plasma Metabolomics and Lipidomics Analyses for Differential Diagnosis of Bladder Cancer and Renal Cell Carcinoma. Frontiers in Oncology, 2020, 10, 717.	2.8	31
11	Proteomics Strategy to Identify Substrates of LNX, a PDZ Domain-containing E3 Ubiquitin Ligase. Journal of Proteome Research, 2012, 11, 4847-4862.	3.7	29
12	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
13	Comprehensive Map and Functional Annotation of Human Pituitary and Thyroid Proteome. Journal of Proteome Research, 2017, 16, 2680-2691.	3.7	27
14	Urinary metabolic variation analysis during pregnancy and application in Gestational Diabetes Mellitus and spontaneous abortion biomarker discovery. Scientific Reports, 2019, 9, 2605.	3.3	22
15	Noninvasive urinary protein signatures associated with colorectal cancer diagnosis and metastasis. Nature Communications, 2022, 13, 2757.	12.8	20
16	A preliminary quantitative proteomic analysis of glioblastoma pseudoprogression. Proteome Science, 2015, 13, 12.	1.7	19
17	UPLC-MS based urine untargeted metabolomic analyses to differentiate bladder cancer from renal cell carcinoma. BMC Cancer, 2019, 19, 1195.	2.6	19
18	Elevated urine histone 4 levels in women with ovarian endometriosis revealed by discovery and parallel reaction monitoring proteomics. Journal of Proteomics, 2019, 204, 103398.	2.4	18

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19	Experimental Study on Differences in Clivus Chordoma Bone Invasion: An iTRAQ-Based Quantitative Proteomic Analysis. PLoS ONE, 2015, 10, e0119523.	2.5	17
20	A comprehensive profile and inter-individual variations analysis of the human normal amniotic fluid proteome. Journal of Proteomics, 2019, 192, 1-9.	2.4	16
21	Differential urinary proteins to diagnose coronary heart disease based on iTRAQ quantitative proteomics. Analytical and Bioanalytical Chemistry, 2019, 411, 2273-2282.	3.7	15
22	Proteomic Study of Aqueous Humor and Its Application in the Treatment of Neovascular Glaucoma. Frontiers in Molecular Biosciences, 2020, 7, 587677.	3.5	15
23	Comparative proteomic analysis of the influence of gender and acid stimulation on normal human saliva using LC/MS/MS. Proteomics - Clinical Applications, 2017, 11, 1600142.	1.6	13
24	Screening E3 Substrates Using a Live Phage Display Library. PLoS ONE, 2013, 8, e76622.	2.5	12
25	A qualitative and quantitative evaluation of the peptide characteristics of microwaveâ€•and ultrasoundâ€•assisted digestion in discovery and targeted proteomic analyses. Rapid Communications in Mass Spectrometry, 2017, 31, 1353-1362.	1.5	12
26	Proteomic Analysis of Liver Proteins in a Rat Model of Chronic Restraint Stress-Induced Depression. BioMed Research International, 2017, 2017, 1-14.	1.9	12
27	Analysis of the differential urinary protein profile in IgA nephropathy patients of Uygur ethnicity. BMC Nephrology, 2018, 19, 358.	1.8	12
28	Data for a comprehensive map and functional annotation of the human cerebrospinal fluid proteome. Data in Brief, 2015, 3, 103-107.	1.0	11
29	Cytoplasmic RAD23B interacts with CORO1C to synergistically promote colorectal cancer progression and metastasis. Cancer Letters, 2021, 516, 13-27.	7.2	11
30	Urinary protein biomarkers for pediatric medulloblastoma. Journal of Proteomics, 2020, 225, 103832.	2.4	10
31	Differential proteome analysis of hippocampus and temporal cortex using label-free based 2D-LC-MS/MS. Journal of Proteomics, 2017, 165, 26-34.	2.4	8
32	GIPC2 is an endocrine-specific tumor suppressor gene for both sporadic and hereditary tumors of RET- and SDHB-, but not VHL-associated clusters of pheochromocytoma/paraganglioma. Cell Death and Disease, 2021, 12, 444.	6.3	8
33	Evaluation of Urinary Proteome Library Generation Methods on Dataâ€•Independent Acquisition MS Analysis and its Application in Normal Urinary Proteome Analysis. Proteomics - Clinical Applications, 2019, 13, e1800152.	1.6	7
34	Investigation of Plasma Metabolic and Lipidomic Characteristics of a Chinese Cohort and a Pilot Study of Renal Cell Carcinoma Biomarker. Frontiers in Oncology, 2020, 10, 1507.	2.8	7
35	Proteome Characterization of Glaucoma Aqueous Humor. Molecular and Cellular Proteomics, 2021, 20, 100117.	3.8	7
36	Comprehensive map and functional annotation of the mouse white adipose tissue proteome. PeerJ, 2019, 7, e7352.	2.0	7

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37	A Global Multiregional Proteomic Map of the Human Cerebral Cortex. Genomics, Proteomics and Bioinformatics, 2022, 20, 614-632.	6.9	6
38	Differential urinary proteomics analysis of myocardial infarction using iTRAQ quantification. Molecular Medicine Reports, 2019, 19, 3972-3988.	2.4	5
39	A qualitative and quantitative analysis of the human gingival crevicular fluid proteome and metaproteome. Proteomics, 2021, 21, e2000321.	2.2	5
40	Lipoprotein proteome profile: novel insight into hyperlipidemia. Clinical and Translational Medicine, 2021, 11, e361.	4.0	4
41	Alteration of lung tissues proteins in birch pollen induced asthma mice before and after SCIT. PLoS ONE, 2021, 16, e0258051.	2.5	3
42	Evaluation of machine learning models on protein level inference from prioritized RNA features. Briefings in Bioinformatics, 2022, 23, .	6.5	3
43	Qualitative and quantitative proteomic and metaproteomic analyses of healthy human urine sediment. Proteomics - Clinical Applications, 2022, 16, e2100007.	1.6	2
44	Diagnostic Potential of Plasma IgA1 O-Glycans in Discriminating IgA Nephropathy From Other Glomerular Diseases and Healthy Participants. Frontiers in Molecular Biosciences, 2022, 9, 871615.	3.5	2
45	96DRA-Urine: A high throughput sample preparation method for urinary proteome analysis. Journal of Proteomics, 2022, 257, 104529.	2.4	2
46	Special electromagnetic field-treated water and far-infrared radiation alleviates lipopolysaccharide-induced acute respiratory distress syndrome in rats by regulating haptoglobin. Bioengineered, 2021, 12, 6808-6820.	3.2	1
47	Aqueous humor proteomic analysis of acute angle-closure glaucoma with visual field loss. Annals of Translational Medicine, 2021, 9, 0-0.	1.7	1
48	The urinary biomarker database. FASEB Journal, 2011, 25, .	0.5	0
49	Fast Fix, Fish and Filter, 4Facts strategy to identify real time protein€protein interactions in situ with few false positives. FASEB Journal, 2013, 27, 810.2.	0.5	0
50	Urine metabolomics and proteomics for bladder cancer prediction by LC/MS based strategy. FASEB Journal, 2020, 34, 1-1.	0.5	0
51	LC€MS€based urine metabolomics analyses for early diagnosis of medulloblastoma. FASEB Journal, 2020, 34, 1-1.	0.5	0
52	A Probe into the Intervention Mechanism of Yiqi Huayu Jiedu Decoction on TLR4/NLRP3 Signal Pathway in Lipopolysaccharide-Induced Acute Respiratory Distress Syndrome (ARDS) Rats. Evidence-based Complementary and Alternative Medicine, 2022, 2022, 1-11.	1.2	0