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	Qualitative and quantitative proteomic and metaproteomic analyses of healthy human urine sediment. Proteomics - Clinical Applications, 2022, 16, e2100007.	1.6	2
2	A Global Multiregional Proteomic Map of the Human Cerebral Cortex. Genomics, Proteomics and Bioinformatics, 2022, 20, 614-632.	6.9	6
3	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
4	Evaluation of machine learning models on protein level inference from prioritized RNA features. Briefings in Bioinformatics, 2022, 23, .	6.5	3
5	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
6	96DRA-Urine: A high throughput sample preparation method for urinary proteome analysis. Journal of Proteomics, 2022, 257, 104529.	2.4	2
7	Noninvasive urinary protein signatures associated with colorectal cancer diagnosis and metastasis. Nature Communications, 2022, 13, 2757.	12.8	20
8	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
9	Lipoprotein proteome profile: novel insight into hyperlipidemia. Clinical and Translational Medicine, 2021, 11, e361.	4.0	4
10	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
11	Cytoplasmic RAD23B interacts with CORO1C to synergistically promote colorectal cancer progression and metastasis. Cancer Letters, 2021, 516, 13-27.	7.2	11
12	A qualitative and quantitative analysis of the human gingival crevicular fluid proteome and metaproteome. Proteomics, 2021, 21, e2000321.	2.2	5
13	Proteome Characterization of Glaucoma Aqueous Humor. Molecular and Cellular Proteomics, 2021, 20, 100117.	3.8	7
14	Aqueous humor proteomic analysis of acute angle-closure glaucoma with visual field loss. Annals of Translational Medicine, 2021, 9, 0-0.	1.7	1
15	Alteration of lung tissues proteins in birch pollen induced asthma mice before and after SCIT. PLoS ONE, 2021, 16, e0258051.	2.5	3
16	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
17	Proteomic Study of Aqueous Humor and Its Application in the Treatment of Neovascular Glaucoma. Frontiers in Molecular Biosciences, 2020, 7, 587677.	3.5	15
18	Urinary protein biomarkers for pediatric medulloblastoma. Journal of Proteomics, 2020, 225, 103832.	2.4	10

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19	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
20	Urine metabolomics and proteomics for bladder cancer prediction by LC/MS based strategy. FASEB Journal, 2020, 34, 1-1.	0.5	0
21	LC‑MS‑based urine metabolomics analyses for early diagnosis of medulloblastoma. FASEB Journal, 2020, 34, 1-1.	0.5	0
22	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
23	Differential urinary proteomics analysis of myocardial infarction using iTRAQ quantification. Molecular Medicine Reports, 2019, 19, 3972-3988.	2.4	5
24	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
25	Evaluation of Urinary Proteome Library Generation Methods on Data‑Independent Acquisition MS Analysis and its Application in Normal Urinary Proteome Analysis. Proteomics - Clinical Applications, 2019, 13, e1800152.	1.6	7
26	Comprehensive Analysis of Individual Variation in the Urinary Proteome Revealed Significant Gender Differences. Molecular and Cellular Proteomics, 2019, 18, 1110-1122.	3.8	50
27	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
28	Differential urinary proteins to diagnose coronary heart disease based on iTRAQ quantitative proteomics. Analytical and Bioanalytical Chemistry, 2019, 411, 2273-2282.	3.7	15
29	UPLC-MS based urine untargeted metabolomic analyses to differentiate bladder cancer from renal cell carcinoma. BMC Cancer, 2019, 19, 1195.	2.6	19
30	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
31	Comprehensive map and functional annotation of the mouse white adipose tissue proteome. PeerJ, 2019, 7, e7352.	2.0	7
32	Analysis of the differential urinary protein profile in IgA nephropathy patients of Uygur ethnicity. BMC Nephrology, 2018, 19, 358.	1.8	12
33	Metabolomics of Non-muscle Invasive Bladder Cancer: Biomarkers for Early Detection of Bladder Cancer. Frontiers in Oncology, 2018, 8, 494.	2.8	43
34	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
35	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
36	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

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37	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
38	Dynamic changes of urine proteome in a Walker 256 tumorâ€•bearing rat model. Cancer Medicine, 2017, 6, 2713-2722.	2.8	48
39	A comprehensive analysis and annotation of human normal urinary proteome. Scientific Reports, 2017, 7, 3024.	3.3	127
40	Comprehensive Map and Functional Annotation of Human Pituitary and Thyroid Proteome. Journal of Proteome Research, 2017, 16, 2680-2691.	3.7	27
41	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
42	A novel TP53 pathway influences the HGS-mediated exosome formation in colorectal cancer. Scientific Reports, 2016, 6, 28083.	3.3	45
43	Differential urinary glycoproteome analysis of type 2 diabetic nephropathy using 2D-LCâ€"MS/MS and iTRAQ quantification. Journal of Translational Medicine, 2015, 13, 371.	4.4	29
44	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
45	A comprehensive map and functional annotation of the normal human cerebrospinal fluid proteome. Journal of Proteomics, 2015, 119, 90-99.	2.4	57
46	A preliminary quantitative proteomic analysis of glioblastoma pseudoprogression. Proteome Science, 2015, 13, 12.	1.7	19
47	Data for a comprehensive map and functional annotation of the human cerebrospinal fluid proteome. Data in Brief, 2015, 3, 103-107.	1.0	11
48	Experimental Study on Differences in Clivus Chordoma Bone Invasion: An iTRAQ-Based Quantitative Proteomic Analysis. PLoS ONE, 2015, 10, e0119523.	2.5	17
49	Screening E3 Substrates Using a Live Phage Display Library. PLoS ONE, 2013, 8, e76622.	2.5	12
50	Fast Fix, Fish and Filter, 4Facts strategy to identify real time proteinâ€•protein interactions in situ with few false positives. FASEB Journal, 2013, 27, 810.2.	0.5	0
51	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
52	The urinary biomarker database. FASEB Journal, 2011, 25, .	0.5	0