

Wei Yan

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

2,316
citations

279778

23
h-index

315719

38
g-index

40
all docs

40
docs citations

40
times ranked

3770
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical and radiological features of medullary infarction caused by spontaneous vertebral artery dissection. <i>Stroke and Vascular Neurology</i> , 2022, 7, 245-250.	3.3	1
2	Extracellular Vesicles, New Players in Sepsis and Acute Respiratory Distress Syndrome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 853840.	3.9	5
3	Comprehensive analysis of O-glycosylation of amyloid precursor protein (APP) using targeted and multi-fragmentation MS strategy. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129954.	2.4	6
4	Towards early risk biomarkers: serum metabolic signature in childhood predicts cardio-metabolic risk in adulthood. <i>EBioMedicine</i> , 2021, 72, 103611.	6.1	14
5	Data independent acquisition-mass spectrometry (DIA-MS)-based comprehensive profiling of bone metastatic cancers revealed molecular fingerprints to assist clinical classifications for bone metastasis of unknown primary (BMUP). <i>Translational Cancer Research</i> , 2020, 9, 2390-2401.	1.0	3
6	O-linked N-acetylgalactosamine modification is present on the tumor suppressor p53. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129635.	2.4	5
7	Immune Cell-Derived Exosomes in the Cancer-Immunity Cycle. <i>Trends in Cancer</i> , 2020, 6, 506-517.	7.4	95
8	Deciphering tissue-based proteome signatures revealed novel subtyping and prognostic markers for thymic epithelial tumors. <i>Molecular Oncology</i> , 2020, 14, 721-741.	4.6	9
9	Comprehensive Map of the <i>Artemisia annua</i> Proteome and Quantification of Differential Protein Expression in Chemotypes Producing High versus Low Content of Artemisinin. <i>Proteomics</i> , 2020, 20, e1900310.	2.2	6
10	Data-independent acquisition-based quantitative proteomic analysis reveals differences in host immune response of peripheral blood mononuclear cells to sepsis. <i>Scandinavian Journal of Immunology</i> , 2019, 89, e12748.	2.7	12
11	Discovering Protein Biomarkers from Clinical Peripheral Blood Mononuclear Cells Using Data-Independent Acquisition Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 1959, 151-161.	0.9	0
12	Interplay between the bacterial protein deacetylase CobB and the second messenger cAMP•GMP. <i>EMBO Journal</i> , 2019, 38, e100948.	7.8	28
13	In-Depth Characterization of Mass Spectrometry-Based Proteomic Profiles Revealed Novel Signature Proteins Associated with Liver Metastatic Colorectal Cancers. <i>Analytical Cellular Pathology</i> , 2019, 1-9.	1.4	7
14	Exosomal proteome analysis of human plasma to monitor sepsis progression. <i>Biochemical and Biophysical Research Communications</i> , 2018, 499, 856-861.	2.1	30
15	Extraction, detection, and profiling of serum biomarkers using designed Fe ₃ O ₄ @SiO ₂ @HA core-shell particles. <i>Nano Research</i> , 2018, 11, 68-79.	10.4	65
16	Investigation of an optimal lysis method for the study of thymus and thymoma by mass spectrometry-based proteomics. <i>Translational Cancer Research</i> , 2018, 7, 391-400.	1.0	2
17	The Ser/Thr Protein Kinase Protein-Protein Interaction Map of <i>M. tuberculosis</i> *. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1491-1506.	3.8	39
18	Differential expression of ST6GAL1 in the tumor progression of colorectal cancer. <i>Biochemical and Biophysical Research Communications</i> , 2017, 486, 1090-1096.	2.1	21

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19	Systematic Identification of Mycobacterium tuberculosis Effectors Reveals that BfrB Suppresses Innate Immunity. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2243-2253.	3.8	18
20	Micro<scp>RNA</scp>â€137 and micro<scp>RNA</scp>â€195* inhibit vasculogenesis in brain arteriovenous malformations. <i>Annals of Neurology</i> , 2017, 82, 371-384.	5.3	33
21	Interleukin-6 Induced â€Acuteâ€-Phenotypic Microenvironment Promotes Th1 Anti-Tumor Immunity in Cryo-Thermal Therapy Revealed By Shotgun and Parallel Reaction Monitoring Proteomics. <i>Theranostics</i> , 2016, 6, 773-794.	10.0	46
22	Systematic identification of arsenic-binding proteins reveals that hexokinase-2 is inhibited by arsenic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15084-15089.	7.1	126
23	Metalloproteinase-mediated Shedding of Integrin Î2 Promotes Macrophage Efflux from Inflammatory Sites. <i>Journal of Biological Chemistry</i> , 2012, 287, 4581-4589.	3.4	43
24	Argininosuccinate synthase conditions the response to acute and chronic ethanol-induced liver injury in mice. <i>Hepatology</i> , 2012, 55, 1596-1609.	7.3	49
25	Index-ion Triggered MS2 Ion Quantification: A Novel Proteomics Approach for Reproducible Detection and Quantification of Targeted Proteins in Complex Mixtures. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005611.	3.8	26
26	Prequipsâ€”an extensible software platform for integration, visualization and analysis of LC-MS/MS proteomics data. <i>Bioinformatics</i> , 2009, 25, 682-683.	4.1	12
27	Evolution of organelle-associated protein profiling. <i>Journal of Proteomics</i> , 2009, 72, 4-11.	2.4	39
28	Quantitative Proteomic Analysis to Profile Dynamic Changes in the Spatial Distribution of Cellular Proteins. <i>Methods in Molecular Biology</i> , 2008, 432, 389-401.	0.9	30
29	Mass spectrometry-based quantitative proteomic profiling. <i>Briefings in Functional Genomics & Proteomics</i> , 2005, 4, 27-38.	3.8	92
30	A Dataset of Human Liver Proteins Identified by Protein Profiling Via Isotope-coded Affinity Tag (ICAT) and Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 1039-1041.	3.8	56
31	Chemical probes and tandem mass spectrometry: a strategy for the quantitative analysis of proteomes and subproteomes. <i>Current Opinion in Chemical Biology</i> , 2004, 8, 66-75.	6.1	144
32	Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry. <i>Genome Biology</i> , 2004, 6, R9.	9.6	252
33	System-based proteomic analysis of the interferon response in human liver cells. <i>Genome Biology</i> , 2004, 5, R54.	9.6	63
34	The regulation of hepatitis C virus (HCV) internal ribosome-entry site-mediated translation by HCV replicons and nonstructural proteins. <i>Journal of General Virology</i> , 2003, 84, 535-543.	2.9	64
35	Control of PERK eIF2Â kinase activity by the endoplasmic reticulum stress-induced molecular chaperone P58IPK. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15920-15925.	7.1	330
36	Inactivation of the PKR Protein Kinase and Stimulation of mRNA Translation by the Cellular Co-Chaperone P58IPK Does Not Require J Domain Function. <i>Biochemistry</i> , 2002, 41, 4938-4945.	2.5	28

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37	The Glycine-Phenylalanine-Rich Region Determines the Specificity of the Yeast Hsp40 Sis1. <i>Molecular and Cellular Biology</i> , 1999, 19, 7751-7758.	2.3	147
38	Zuotin, a ribosome-associated DnaJmolecular chaperone. <i>EMBO Journal</i> , 1998, 17, 4809-4817.	7.8	150
39	Functional Interaction of Cytosolic hsp70 and a DnaJ-Related Protein, Ydj1p, in Protein Translocation In Vivo. <i>Molecular and Cellular Biology</i> , 1996, 16, 4378-4386.	2.3	220