

List of Publications by Year in descending order

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95	4,020	25	58
papers	citations	h-index	g-index
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all docs	docs citations	times ranked	citing authors

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#	Article	IF	CITATIONS
1	Fluorescein-labeled ThUBD probe for super-sensitive visualization of polyubiquitination signal in situ cells. Talanta, 2023, 253, 123564.	5.5	2
2	Improving Clinician-Patient Communication Alleviates Stigma in Patients With Functional Dyspepsia Receiving Antidepressant Treatment. Journal of Neurogastroenterology and Motility, 2022, 28, 95-103.	2.4	5
3	Recombinant HNP-1 Produced by Escherichia coli Triggers Bacterial Apoptosis and Exhibits Antibacterial Activity against Drug-Resistant Bacteria. Microbiology Spectrum, 2022, , e0086021.	3.0	2
4	Proteomic and metabolomic profiling of urine uncovers immune responses in patients with COVID-19. Cell Reports, 2022, 38, 110271.	6.4	66
5	Deep N-terminomics of Mycobacterium tuberculosis H37Rv extensively correct annotated encoding genes. Genomics, 2022, 114, 292-304.	2.9	3
6	Regulation of mitophagy by metformin improves the structure and function of retinal ganglion cells following excitotoxicity-induced retinal injury. Experimental Eye Research, 2022, 217, 108979.	2.6	5
7	Benchmarking Cleavable Biotin Tags for Peptide-Centric Chemoproteomics. Journal of Proteome Research, 2022, 21, 1349-1358.	3.7	15
8	A proteomics strategy for the identification of multiple sites in sulfur mustard–modified HSA and screening potential biomarkers for retrospective analysis of exposed human plasma. Analytical and Bioanalytical Chemistry, 2022, 414, 4179-4188.	3.7	2
9	Ac-LysargiNase efficiently helps genome reannotation of Mycolicibacterium smegmatis MC2 155. Journal of Proteomics, 2022, 264, 104622.	2.4	1
10	Quantitative phosphoproteomics reveal cellular responses from caffeine, coumarin and quercetin in treated HepG2 cells. Toxicology and Applied Pharmacology, 2022, 449, 116110.	2.8	4
11	Chemically labeled ThUBD permits rapid and super-sensitive imaging of polyubiquitination signals. Analyst, The, 2022, 147, 3434-3443.	3.5	1
12	Serum protein complex profiling reveals heterogeneity of Balanced constitutional population in traditional Chinese medicine through blue native polyacrylamide gel electrophoresis. Annals of Palliative Medicine, 2021, 10, 1703-1716.	1.2	0
13	Deubiquitinase Ubp3 enhances the proteasomal degradation of key enzymes in sterol homeostasis. Journal of Biological Chemistry, 2021, 296, 100348.	3.4	5
14	Mass-Spectrometry-Based Near-Complete Draft of the <i>Saccharomyces cerevisiae</i> Proteome. Journal of Proteome Research, 2021, 20, 1328-1340.	3.7	13
15	Anemarrhena asphodeloides modulates gut microbiota and restores pancreatic function in diabetic rats. Biomedicine and Pharmacotherapy, 2021, 133, 110954.	5.6	19
16	Serum-Derived Exosomal Proteins as Potential Candidate Biomarkers for Hepatocellular Carcinoma. ACS Omega, 2021, 6, 827-835.	3.5	16
17	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
18	DeepDigest: Prediction of Protein Proteolytic Digestion with Deep Learning. Analytical Chemistry, 2021, 93, 6094-6103.	6.5	23

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19	Cell subtypes and immune dysfunction in peritoneal fluid of endometriosis revealed by single-cell RNA-sequencing. Cell and Bioscience, 2021, 11, 98.	4.8	31
20	Proteogenomics Study of <i>Blastobotrys adeninivorans</i> TMCC 70007—A Dominant Yeast in the Fermentation Process of Pu-erh Tea. Journal of Proteome Research, 2021, 20, 3290-3304.	3.7	6
21	SARS-CoV-2 infection in the mouse olfactory system. Cell Discovery, 2021, 7, 49.	6.7	47
22	Translatomic profiling reveals novel self-restricting virus-host interactions during HBV infection. Journal of Hepatology, 2021, 75, 74-85.	3.7	16
23	Unravelling the role of bandâ€offset landscape on the recombination zone dynamics in perovskite lightâ€emitting diodes. Nano Select, 2021, 2, 624-631.	3.7	6
24	Association of Myometrial Invasion With Lymphovascular Space Invasion, Lymph Node Metastasis, Recurrence, and Overall Survival in Endometrial Cancer: A Meta-Analysis of 79 Studies With 68,870 Patients. Frontiers in Oncology, 2021, 11, 762329.	2.8	12
25	Multiomics interrogation into HBV (Hepatitis B virus)-host interaction reveals novel coding potential in human genome, and identifies canonical and non-canonical proteins as host restriction factors against HBV. Cell Discovery, 2021, 7, 105.	6.7	9
26	Development of a novel miR-3648-related gene signature as a prognostic biomarker in esophageal adenocarcinoma. Annals of Translational Medicine, 2021, 9, 1702-1702.	1.7	2
27	Specific and Unbiased Detection of Polyubiquitination via a Sensitive Non-Antibody Approach. Analytical Chemistry, 2020, 92, 1074-1080.	6.5	7
28	Quantitative Proteomics Combined with Two Genetic Strategies for Screening Substrates of Ubiquitin Ligase Hrt3. Journal of Proteome Research, 2020, 19, 493-502.	3.7	3
29	Comparison of subsequent pregnancy outcomes after surgery for adnexal masses performed in the first and second trimester of pregnancy. International Journal of Gynecology and Obstetrics, 2020, 148, 305-309.	2.3	5
30	Ubiquitin Linkage Specificity of Deubiquitinases Determines Cyclophilin Nuclear Localization and Degradation. IScience, 2020, 23, 100984.	4.1	5
31	Open-pFind Verified Four Missing Proteins from Multi-Tissues. Journal of Proteome Research, 2020, 19, 4808-4814.	3.7	3
32	Unambiguous Phosphosite Localization through the Combination of Trypsin and LysargiNase Mirror Spectra in a Large-Scale Phosphoproteome Study. Journal of Proteome Research, 2020, 19, 2185-2194.	3.7	7
33	Novel variants associated with Stargardt disease in Chinese patients. Gene, 2020, 754, 144890.	2.2	9
34	Quantitative Proteomics Reveals the Development of HBV-Associated Glomerulonephritis Triggered by the Downregulation of SLC7A7. Journal of Proteome Research, 2020, 19, 1556-1564.	3.7	7
35	Urine proteome of COVID-19 patients. Urine, 2020, 2, 1-8.	4.0	51
36	Breast non-mass-like lesions on contrast-enhanced ultrasonography: Feature analysis, breast image reporting and data system classification assessment. World Journal of Clinical Cases, 2020, 8, 700-712.	0.8	13

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37	Proteomics Links Ubiquitin Chain Topology Change to Transcription Factor Activation. Molecular Cell, 2019, 76, 126-137.e7.	9.7	24
38	<p>Comparisons of the efficacy and recurrence of adenomyomectomy for severe uterine diffuse adenomyosis via laparotomy versus laparoscopy: a long-term result in a single institution</p> . Journal of Pain Research, 2019, Volume 12, 1917-1924.	2.0	24
39	Open-pFind Enhances the Identification of Missing Proteins from Human Testis Tissue. Journal of Proteome Research, 2019, 18, 4189-4196.	3.7	13
40	Genetic and Clinical Findings in a Large Cohort of Chinese Patients with Suspected Retinitis Pigmentosa. Ophthalmology, 2019, 126, 1549-1556.	5.2	78
41	Racioethnic diversity in the dynamics of the vaginal microbiome during pregnancy. Nature Medicine, 2019, 25, 1001-1011.	30.7	204
42	LysargiNase enhances protein identification on the basis of trypsin on formalinâ€fixed paraffinâ€embedded samples. Rapid Communications in Mass Spectrometry, 2019, 33, 1381-1389.	1.5	6
43	Recombinant expression, purification and characterization of acetylated LysargiNase from <scp><i>Escherichia coli</i></scp> with high activity and stability. Rapid Communications in Mass Spectrometry, 2019, 33, 1067-1075.	1.5	6
44	Notch signalling regulates steroidogenesis in mouse ovarian granulosa cells. Reproduction, Fertility and Development, 2019, 31, 1091.	0.4	12
45	Ac-LysargiNase Complements Trypsin for the Identification of Ubiquitinated Sites. Analytical Chemistry, 2019, 91, 15890-15898.	6.5	5
46	Quantitative proteomics reveals mitochondrial respiratory chain as a dominant target for carbon ion radiation: Delayed reactive oxygen species generation caused DNA damage. Free Radical Biology and Medicine, 2019, 130, 436-445.	2.9	23
47	Precision De Novo Peptide Sequencing Using Mirror Proteases of Ac-LysargiNase and Trypsin for Large-scale Proteomics. Molecular and Cellular Proteomics, 2019, 18, 773-785.	3.8	36
48	CDK5RAP3, a UFL1 substrate adaptor, is critical for liver development. Development (Cambridge), 2019, 146, .	2.5	49
49	Comprehensive identification of peptides in tandem mass spectra using an efficient open search engine. Nature Biotechnology, 2018, 36, 1059-1061.	17.5	275
50	Multiproteases Combined with High-pH Reverse-Phase Separation Strategy Verified Fourteen Missing Proteins in Human Testis Tissue. Journal of Proteome Research, 2018, 17, 4171-4177.	3.7	20
51	Digging for Missing Proteins Using Low-Molecular-Weight Protein Enrichment and a "Mirror Protease―Strategy. Journal of Proteome Research, 2018, 17, 4178-4185.	3.7	12
52	Clinical analysis of 50 patients with heterotopic pregnancy after ovulation induction or embryo transfer. European Journal of Medical Research, 2018, 23, 17.	2.2	21
53	Proteomic Analysis and NIR-II Imaging of MCM2 Protein in Hepatocellular Carcinoma. Journal of Proteome Research, 2018, 17, 2428-2439.	3.7	51
54	Enrichment-Based Proteogenomics Identifies Microproteins, Missing Proteins, and Novel smORFs in <i>Saccharomyces cerevisiae</i> . Journal of Proteome Research, 2018, 17, 2335-2344.	3.7	35

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55	Multi-omics analyses reveal metabolic alterations regulated by hepatitis B virus core protein in hepatocellular carcinoma cells. Scientific Reports, 2017, 7, 41089.	3.3	39
56	A rapid and easy protein Nâ€ŧerminal profiling strategy using (<i>N</i> ‣uccinimidyloxycarbonylmethyl)tris(2,4,6â€ŧrimethoxyphenyl)phosphonium bromide (TMPP) labeling and StageTip. Proteomics, 2017, 17, 1600481.	2.2	14
57	Highâ€coverage proteomics reveals methionine auxotrophy in <i>Deinococcus radiodurans</i> . Proteomics, 2017, 17, 1700072.	2.2	7
58	Multi-Protease Strategy Identifies Three PE2 Missing Proteins in Human Testis Tissue. Journal of Proteome Research, 2017, 16, 4352-4363.	3.7	21
59	Identification of Missing Proteins in the Phosphoproteome of Kidney Cancer. Journal of Proteome Research, 2017, 16, 4364-4373.	3.7	19
60	Hepatitis B Virus X Protein Stimulates Proliferation, Wound Closure and Inhibits Apoptosis of HuH-7 Cells via CDC42. International Journal of Molecular Sciences, 2017, 18, 586.	4.1	21
61	Hepatitis B virus X induces inflammation and cancer in mice liver through dysregulation of cytoskeletal remodeling and lipid metabolism. Oncotarget, 2016, 7, 70559-70574.	1.8	30
62	Congenital Heart Defects in the United States. Circulation, 2016, 134, 101-109.	1.6	507
63	Recombinant acetylated trypsin demonstrates superior stability and higher activity than commercial products in quantitative proteomics studies . Rapid Communications in Mass Spectrometry, 2016, 30, 1059-1066.	1.5	21
64	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). Molecular and Cellular Proteomics, 2016, 15, 1381-1396.	3.8	15
65	Searching Missing Proteins Based on the Optimization of Membrane Protein Enrichment and Digestion Process. Journal of Proteome Research, 2016, 15, 4020-4029.	3.7	15
66	Deep Coverage Proteomics Identifies More Low-Abundance Missing Proteins in Human Testis Tissue with Q-Exactive HF Mass Spectrometer. Journal of Proteome Research, 2016, 15, 3988-3997.	3.7	38
67	Comparative Proteomic Analysis of Buffalo Oocytes Matured in vitro Using iTRAQ Technique. Scientific Reports, 2016, 6, 31795.	3.3	21
68	iTRAQ-Based Membrane Proteomics Reveals Plasma Membrane Proteins Change During HepaRG Cell Differentiation. Journal of Proteome Research, 2016, 15, 4245-4257.	3.7	1
69	Recombinant expression, refolding, purification and characterization of Pseudomonas aeruginosa protease IV in Escherichia coli. Protein Expression and Purification, 2016, 126, 69-76.	1.3	16
70	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). Molecular and Cellular Proteomics, 2016, 15, 1381-1396.	3.8	44
71	Quantitative Proteomics Reveals Membrane Protein-Mediated Hypersaline Sensitivity and Adaptation in Halophilic <i>Nocardiopsis xinjiangensis</i> . Journal of Proteome Research, 2016, 15, 68-85.	3.7	35
72	Quantitative proteomics reveals FLNC as a potential progression marker for the development of hepatocellular carcinoma. Oncotarget, 2016, 7, 68242-68252.	1.8	28

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73	Development of Gel-Filter Method for High Enrichment of Low-Molecular Weight Proteins from Serum. PLoS ONE, 2015, 10, e0115862.	2.5	13
74	Phosphoproteomic Analysis of the Highly-Metastatic Hepatocellular Carcinoma Cell Line, MHCC97-H. International Journal of Molecular Sciences, 2015, 16, 4209-4225.	4.1	22
75	Special Enrichment Strategies Greatly Increase the Efficiency of Missing Proteins Identification from Regular Proteome Samples. Journal of Proteome Research, 2015, 14, 3680-3692.	3.7	15
76	Evolutionary Characteristics of Missing Proteins: Insights into the Evolution of Human Chromosomes Related to Missing-Protein-Encoding Genes. Journal of Proteome Research, 2015, 14, 4985-4994.	3.7	9
77	Activation of P2X7 receptors decreases the proliferation of murine luteal cells. Reproduction, Fertility and Development, 2015, 27, 1262.	0.4	15
78	Tissue-Based Proteogenomics Reveals that Human Testis Endows Plentiful Missing Proteins. Journal of Proteome Research, 2015, 14, 3583-3594.	3.7	45
79	A note on the false discovery rate of novel peptides in proteogenomics. Bioinformatics, 2015, 31, 3249-3253.	4.1	27
80	Development of a rapid high-efficiency scalable process for acetylated Sus scrofa cationic trypsin production from Escherichia coli inclusion bodies. Protein Expression and Purification, 2015, 116, 120-126.	1.3	22
81	Omics Evidence: Single Nucleotide Variants Transmissions on Chromosome 20 in Liver Cancer Cell Lines. Journal of Proteome Research, 2014, 13, 200-211.	3.7	14
82	Systematic Analyses of the Transcriptome, Translatome, and Proteome Provide a Global View and Potential Strategy for the C-HPP. Journal of Proteome Research, 2014, 13, 38-49.	3.7	60
83	Qualitative and quantitative analysis of the adultDrosophila melanogasterproteome. Proteomics, 2014, 14, 286-290.	2.2	16
84	Systematic Analysis of Missing Proteins Provides Clues to Help Define All of the Protein-Coding Genes on Human Chromosome 1. Journal of Proteome Research, 2014, 13, 114-125.	3.7	21
85	Systematic research on the pretreatment of peptides for quantitative proteomics using a <scp>C</scp> ₁₈ microcolumn. Proteomics, 2013, 13, 2229-2237.	2.2	30
86	Stable Isotope Labeling with Amino Acids in <i>Drosophila</i> for Quantifying Proteins and Modifications. Journal of Proteome Research, 2012, 11, 4403-4412.	3.7	34
87	Pioglitazone: A Promising Therapeutic Tool in Sodium Taurocholate-Induced Severe Acute Pancreatitis. Digestive Diseases and Sciences, 2011, 56, 1082-1089.	2.3	16
88	Systematical Optimization of Reverse-Phase Chromatography for Shotgun Proteomics. Journal of Proteome Research, 2009, 8, 3944-3950.	3.7	163
89	Quantitative Proteomics Reveals the Function of Unconventional Ubiquitin Chains in Proteasomal Degradation. Cell, 2009, 137, 133-145.	28.9	948
90	Systematic Approach for Validating the Ubiquitinated Proteome. Analytical Chemistry, 2008, 80, 4161-4169.	6.5	65

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91	Characterization of Polyubiquitin Chain Structure by Middle-down Mass Spectrometry. Analytical Chemistry, 2008, 80, 3438-3444.	6.5	99
92	A Proteomic Strategy for Quantifying Polyubiquitin Chain Topologies. Israel Journal of Chemistry, 2006, 46, 171-182.	2.3	20
93	Dissecting the ubiquitin pathway by mass spectrometry. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 1940-1947.	2.3	72
94	Research on the protection effect of pioglitazone for non-alcoholic fatty liver disease (NAFLD) in rats. Journal of Zhejiang University: Science B, 2006, 7, 627-633.	2.8	31
95	Morphometric analysis of the immunohistochemical expression of Clara cell 10-kDa protein and surfactant apoproteins A and B in the developing bronchi and bronchioles of human fetuses and neonates. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 1998, 432, 17-25.	2.8	25