Hu Zhou

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Integrated Proteogenomic Characterization of HBV-Related Hepatocellular Carcinoma. Cell, 2019, 179, 561-577.e22.	13.5	629
2	Small-Molecule Targeting of Oncogenic FTO Demethylase in Acute Myeloid Leukemia. Cancer Cell, 2019, 35, 677-691.e10.	7.7	516
3	Meclofenamic acid selectively inhibits FTO demethylation of m6A over ALKBH5. Nucleic Acids Research, 2015, 43, 373-384.	6.5	453
4	Long noncoding RNA LINC00336 inhibits ferroptosis in lung cancer by functioning as a competing endogenous RNA. Cell Death and Differentiation, 2019, 26, 2329-2343.	5.0	365
5	Altered intestinal microbiota–host mitochondria crosstalk in new onset Crohn's disease. Nature Communications, 2016, 7, 13419.	5.8	326
6	YTHDF1 links hypoxia adaptation and non-small cell lung cancer progression. Nature Communications, 2019, 10, 4892.	5.8	256
7	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. Nature Biotechnology, 2019, 37, 314-322.	9.4	254
8	Acetylation of PGK1 promotes liver cancer cell proliferation and tumorigenesis. Hepatology, 2017, 65, 515-528.	3.6	200
9	EGLN1/c-Myc Induced Lymphoid-Specific Helicase Inhibits Ferroptosis through Lipid Metabolic Gene Expression Changes. Theranostics, 2017, 7, 3293-3305.	4.6	199
10	Lipidomics era: Accomplishments and challenges. Mass Spectrometry Reviews, 2010, 29, 877-929.	2.8	161
11	A complex structure of arrestin-2 bound to a G protein-coupled receptor. Cell Research, 2019, 29, 971-983.	5.7	155
12	pFind: a novel database-searching software system for automated peptide and protein identification via tandem mass spectrometry. Bioinformatics, 2005, 21, 3049-3050.	1.8	153
13	Heterogeneous immunogenomic features and distinct escape mechanisms in multifocal hepatocellular carcinoma. Journal of Hepatology, 2020, 72, 896-908.	1.8	124
14	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. Cancer Cell, 2022, 40, 70-87.e15.	7.7	120
15	ERK kinase phosphorylates and destabilizes the tumor suppressor FBW7 in pancreatic cancer. Cell Research, 2015, 25, 561-573.	5.7	112
16	Conformational states of the full-length glucagon receptor. Nature Communications, 2015, 6, 7859.	5.8	110
17	Proteomic analysis of hepatitis B virus-associated hepatocellular carcinoma: Identification of potential tumor markers. Proteomics, 2005, 5, 1125-1139.	1.3	106
18	SARS-CoV-2 envelope protein causes acute respiratory distress syndrome (ARDS)-like pathological damages and constitutes an antiviral target. Cell Research, 2021, 31, 847-860.	5.7	102

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19	A redox mechanism underlying nucleolar stress sensing by nucleophosmin. Nature Communications, 2016, 7, 13599.	5.8	94
20	Missense Mutation in APOC3 within the C-terminal Lipid Binding Domain of Human ApoC-III Results in Impaired Assembly and Secretion of Triacylglycerol-rich Very Low Density Lipoproteins. Journal of Biological Chemistry, 2011, 286, 27769-27780.	1.6	91
21	Characterization of the 3a Protein of SARS-associated Coronavirus in Infected Vero E6 Cells and SARS Patients. Journal of Molecular Biology, 2004, 341, 271-279.	2.0	89
22	The mTOR–S6K pathway links growth signalling to DNA damage response by targeting RNF168. Nature Cell Biology, 2018, 20, 320-331.	4.6	86
23	Advancements in Top-Down Proteomics. Analytical Chemistry, 2012, 84, 720-734.	3.2	80
24	Proteomic Analysis with Integrated Multiple Dimensional Liquid Chromatography/Mass Spectrometry Based on Elution of Ion Exchange Column Using pH Steps. Analytical Chemistry, 2005, 77, 5793-5799.	3.2	75
25	Quantitative Analysis of Severe Acute Respiratory Syndrome (SARS)-associated Coronavirus-infected Cells Using Proteomic Approaches. Molecular and Cellular Proteomics, 2005, 4, 902-913.	2.5	74
26	A High-throughput Approach for Subcellular Proteome. Molecular and Cellular Proteomics, 2004, 3, 441-455.	2.5	71
27	Localized-Statistical Quantification of Human Serum Proteome Associated with Type 2 Diabetes. PLoS ONE, 2008, 3, e3224.	1.1	67
28	Ruthenium-Promoted C–H Activation Reactions between DNA-Conjugated Acrylamide and Aromatic Acids. Organic Letters, 2018, 20, 4764-4768.	2.4	67
29	Phosphoproteome analysis of mouse liver using immobilized metal affinity purification and linear ion trap mass spectrometry. Rapid Communications in Mass Spectrometry, 2004, 18, 2169-2176.	0.7	63
30	Nonsynonymous Mutations within APOB in Human Familial Hypobetalipoproteinemia. Journal of Biological Chemistry, 2010, 285, 6453-6464.	1.6	58
31	The differential protein and lipid compositions of noncaveolar lipid microdomains and caveolae. Cell Research, 2009, 19, 497-506.	5.7	57
32	Global and Site-Specific Effect of Phosphorylation on Protein Turnover. Developmental Cell, 2021, 56, 111-124.e6.	3.1	57
33	Functional analysis of the missense APOC3 mutation Ala23Thr associated with human hypotriglyceridemia. Journal of Lipid Research, 2010, 51, 1524-1534.	2.0	53
34	Rare Cell Proteomic Reactor Applied to Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC)-based Quantitative Proteomics Study of Human Embryonic Stem Cell Differentiation. Molecular and Cellular Proteomics, 2011, 10, S1-S10.	2.5	52
35	Palladium-Promoted DNA-Compatible Heck Reaction. Organic Letters, 2019, 21, 719-723.	2.4	51
36	Metaproteomics: A strategy to study the taxonomy and functionality of the gut microbiota. Journal of Proteomics, 2020, 219, 103737.	1.2	51

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37	Real-Time Analysis on Drug-Antibody Ratio of Antibody-Drug Conjugates for Synthesis, Process Optimization, and Quality Control. Scientific Reports, 2017, 7, 7763.	1.6	50
38	Identification of Glutaminyl Cyclase isoenzyme isoQC as a regulator of SIRPα-CD47 axis. Cell Research, 2019, 29, 502-505.	5.7	49
39	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. Nature Communications, 2020, 11, 5248.	5.8	49
40	A fully automated 2â€Ð LCâ€MS method utilizing online continuous pH and RP gradients for global proteome analysis. Electrophoresis, 2007, 28, 4311-4319.	1.3	47
41	A novel USP9X substrate TTK contributes to tumorigenesis in non-small-cell lung cancer. Theranostics, 2018, 8, 2348-2360.	4.6	46
42	The Liver Connexin32 Interactome Is a Novel Plasma Membrane-Mitochondrial Signaling Nexus. Journal of Proteome Research, 2013, 12, 2597-2610.	1.8	45
43	Non-transition Metal-Mediated Diverse Aryl–Heteroatom Bond Formation of Arylammonium Salts. IScience, 2019, 15, 307-315.	1.9	44
44	Proteomics: From Technology Developments to Biological Applications. Analytical Chemistry, 2009, 81, 4585-4599.	3.2	42
45	Isoformâ€resolved correlation analysis between <scp>mRNA</scp> abundance regulation and protein level degradation. Molecular Systems Biology, 2020, 16, e9170.	3.2	42
46	S100A11 Promotes Liver Steatosis via FOXO1-Mediated Autophagy and Lipogenesis. Cellular and Molecular Gastroenterology and Hepatology, 2021, 11, 697-724.	2.3	42
47	TGF-β1/p65/MAT2A pathway regulates liver fibrogenesis via intracellular SAM. EBioMedicine, 2019, 42, 458-469.	2.7	41
48	Triptolide Induces Cell Killing in Multidrug-Resistant Tumor Cells via CDK7/RPB1 Rather than XPB or p44. Molecular Cancer Therapeutics, 2016, 15, 1495-1503.	1.9	39
49	GIAT4RA functions as a tumor suppressor in non-small cell lung cancer by counteracting Uchl3–mediated deubiquitination of LSH. Oncogene, 2019, 38, 7133-7145.	2.6	39
50	Large-scale identification of human biliary proteins from a cholesterol stone patient using a proteomic approach. Rapid Communications in Mass Spectrometry, 2005, 19, 3569-3578.	0.7	38
51	mChIP-KAT-MS, a method to map protein interactions and acetylation sites for lysine acetyltransferases. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1641-50.	3.3	38
52	Activation of AhR with nuclear IKKα regulates cancer stem-like properties in the occurrence of radioresistance. Cell Death and Disease, 2018, 9, 490.	2.7	38
53	Technological developments in lipidomics. Briefings in Functional Genomics & Proteomics, 2008, 7, 395-409.	3.8	37
54	Label-Free Proteomics Uncovers Energy Metabolism and Focal Adhesion Regulations Responsive for	1.8	37

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55	Selective N-glycan editing on living cell surfaces to probe glycoconjugate function. Nature Chemical Biology, 2020, 16, 766-775.	3.9	37
56	Quantitative proteomic analysis reveals the neuroprotective effects of huperzine <scp>A</scp> for amyloid beta treated neuroblastoma <scp>N</scp> 2a cells. Proteomics, 2013, 13, 1314-1324.	1.3	35
57	Regulation of Septin Dynamics by the Saccharomyces cerevisiae Lysine Acetyltransferase NuA4. PLoS ONE, 2011, 6, e25336.	1.1	33
58	Proteomic reactors and their applications in biology. FEBS Journal, 2011, 278, 3796-3806.	2.2	33
59	Microsome-associated lumenal lipid droplets in the regulation of lipoprotein secretion. Current Opinion in Lipidology, 2013, 24, 160-170.	1.2	33
60	Characterization of Gain-of-Function Mutant Provides New Insights into ClpP Structure. ACS Chemical Biology, 2016, 11, 1964-1972.	1.6	32
61	Lysoâ€form fragment ions facilitate the determination of stereospecificity of diacyl glycerophospholipids. Rapid Communications in Mass Spectrometry, 2011, 25, 205-217.	0.7	31
62	Improved Recovery and Identification of Membrane Proteins from Rat Hepatic Cells using a Centrifugal Proteomic Reactor. Molecular and Cellular Proteomics, 2011, 10, 0111.008425.	2.5	31
63	Mouse embryonic stem cells have increased capacity for replication fork restart driven by the specific Filia-Floped protein complex. Cell Research, 2018, 28, 69-89.	5.7	31
64	Proteomic Profiling of Regionalized Proteins in Rat Epididymis Indicates Consistency between Specialized Distribution and Protein Functions. Journal of Proteome Research, 2006, 5, 299-307.	1.8	30
65	LOXL1 confers antiapoptosis and promotes gliomagenesis through stabilizing BAG2. Cell Death and Differentiation, 2020, 27, 3021-3036.	5.0	30
66	Glycoproteomic Reactor for Human Plasma. Journal of Proteome Research, 2009, 8, 556-566.	1.8	29
67	Gsy, a novel glucansucrase from Leuconostoc mesenteroides, mediates the formation of cell aggregates in response to oxidative stress. Scientific Reports, 2016, 6, 38122.	1.6	29
68	Analytical Aspects of Proteomics: 2009–2010. Analytical Chemistry, 2011, 83, 4407-4426.	3.2	28
69	Two-dimensional gel electrophoresis maps of the proteome and phosphoproteome of primitively cultured rat mesangial cells. Electrophoresis, 2005, 26, 4540-4562.	1.3	27
70	Quantitative analysis of secretome from adipocytes regulated by insulin. Acta Biochimica Et Biophysica Sinica, 2009, 41, 910-921.	0.9	26
71	Analysis of the Subcellular Phosphoproteome Using a Novel Phosphoproteomic Reactor. Journal of Proteome Research, 2010, 9, 1279-1288.	1.8	25
72	Identification of a Novel Function of Adipocyte Plasma Membrane-Associated Protein (APMAP) in Gestational Diabetes Mellitus by Proteomic Analysis of Omental Adipose Tissue. Journal of Proteome Research, 2016, 15, 628-637.	1.8	25

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73	Prefractionation of Proteome by Liquid Isoelectric Focusing Prior to Two-Dimensional Liquid Chromatography Mass Spectrometric Identification. Journal of Proteome Research, 2005, 4, 1256-1264.	1.8	24
74	Andrographolide Sulfonate Attenuates Acute Lung Injury by Reducing Expression of Myeloperoxidase and Neutrophil-Derived Proteases in Mice. Frontiers in Physiology, 2018, 9, 939.	1.3	24
75	The cross-talk between methylation and phosphorylation in lymphoid-specific helicase drives cancer stem-like properties. Signal Transduction and Targeted Therapy, 2020, 5, 197.	7.1	24
76	An intramolecular disulfide bond designed in myoglobin fine-tunes both protein structure and peroxidase activity. Archives of Biochemistry and Biophysics, 2016, 600, 47-55.	1.4	23
77	Discovery of a Potential Plasma Protein Biomarker Panel for Acute-on-Chronic Liver Failure Induced by Hepatitis B Virus. Frontiers in Physiology, 2017, 8, 1009.	1.3	23
78	Structural basis of rifampin inactivation by rifampin phosphotransferase. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3803-3808.	3.3	22
79	DNA methylation modifier LSH inhibits p53 ubiquitination and transactivates p53 to promote lipid metabolism. Epigenetics and Chromatin, 2019, 12, 59.	1.8	22
80	Dissociative role for dorsal hippocampus in mediating heroin selfâ€administration and relapse through CDK5 and RhoB signaling revealed by proteomic analysis. Addiction Biology, 2017, 22, 1731-1742.	1.4	21
81	Discovery of a subtype-selective, covalent inhibitor against palmitoylation pocket of TEAD3. Acta Pharmaceutica Sinica B, 2021, 11, 3206-3219.	5.7	21
82	Proteomic analysis of minute amount of colonic biopsies by enteroscopy sampling. Biochemical and Biophysical Research Communications, 2016, 476, 286-292.	1.0	20
83	Leflunomide Increases Hepatic Exposure to Methotrexate and Its Metabolite by Differentially Regulating Multidrug Resistance–Associated Protein Mrp2/3/4 Transporters via Peroxisome Proliferator–Activated Receptor α Activation. Molecular Pharmacology, 2018, 93, 563-574.	1.0	19
84	Quantitative Proteomic Study Reveals Up-Regulation of cAMP Signaling Pathway-Related Proteins in Mild Traumatic Brain Injury. Journal of Proteome Research, 2018, 17, 858-869.	1.8	19
85	ITCH nuclear translocation and H1.2 polyubiquitination negatively regulate the DNA damage response. Nucleic Acids Research, 2019, 47, 824-842.	6.5	19
86	Ironâ€induced energy supply deficiency and mitochondrial fragmentation in neurons. Journal of Neurochemistry, 2018, 147, 816-830.	2.1	18
87	SCFFBXW7/CSK3Î ² -Mediated GFI1 Degradation Suppresses Proliferation of Gastric Cancer Cells. Cancer Research, 2019, 79, 4387-4398.	0.4	18
88	Exploring biological basis of Syndrome differentiation in coronary heart disease patients with two distinct Syndromes by integrated multi-omics and network pharmacology strategy. Chinese Medicine, 2021, 16, 109.	1.6	18
89	Analysis of low-abundance proteins using the proteomic reactor with pH fractionation. Talanta, 2010, 80, 1526-1531.	2.9	16
90	Highly sensitive detection of S-nitrosylated proteins by capillary gel electrophoresis with laser induced fluorescence. Journal of Chromatography A, 2011, 1218, 6756-6762.	1.8	16

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91	A novel short-term high-lactose culture approach combined with a matrix-assisted laser desorption ionization-time of flight mass spectrometry assay for differentiating Escherichia coli and Shigella species using artificial neural networks. PLoS ONE, 2019, 14, e0222636.	1.1	16
92	pVHL mediates K63-linked ubiquitination of IKKβ, leading to IKKβ inactivation. Cancer Letters, 2016, 383, 1-8.	3.2	15
93	Combination of online enzyme digestion with stable isotope labeling for highâ€ŧhroughput quantitative proteome analysis. Proteomics, 2012, 12, 3129-3137.	1.3	14
94	Quantitative proteomic analysis of mice corneal tissues reveals angiogenesis-related proteins involved in corneal neovascularization. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 787-793.	1.1	14
95	Recent technological developments in proteomics shed new light on translational research on diabetic microangiopathy. FEBS Journal, 2013, 280, 5668-5681.	2.2	13
96	Identification of a USP9X Substrate NFX1-123 by SILAC-Based Quantitative Proteomics. Journal of Proteome Research, 2019, 18, 2654-2665.	1.8	13
97	Dynamics of Post-Translational Modification Inspires Drug Design in the Kinase Family. Journal of Medicinal Chemistry, 2021, 64, 15111-15125.	2.9	13
98	Development of Online pH Gradient-Eluted Strong Cation Exchange Nanoelectrospray-Tandem Mass Spectrometry for Proteomic Analysis Facilitating Basic and Histidine-Containing Peptides Identification. Analytical Chemistry, 2016, 88, 583-591.	3.2	12
99	SILAC-based quantitative proteomic analysis of the livers of spontaneous obese and diabetic rhesus monkeys. American Journal of Physiology - Endocrinology and Metabolism, 2018, 315, E294-E306.	1.8	12
100	Analysis of Microdissected Cells by Two-Dimensional LC-MS Approaches. Methods in Molecular Biology, 2008, 428, 193-208.	0.4	11
101	Extracellular Signal-regulated Kinases (ERKs) Phosphorylate Lin28a Protein to Modulate P19 Cell Proliferation and Differentiation. Journal of Biological Chemistry, 2017, 292, 3970-3976.	1.6	11
102	Quantitative Proteomics Reveals the Protective Effects of Huangqi Decoction Against Acute Cholestatic Liver Injury by Inhibiting the NF-κB/IL-6/STAT3 Signaling Pathway. Journal of Proteome Research, 2020, 19, 677-687.	1.8	11
103	Allosteric Regulation of Hsp90α's Activity by Small Molecules Targeting the Middle Domain of the Chaperone. IScience, 2020, 23, 100857.	1.9	11
104	A novel IncRNA Discn fine-tunes replication protein A (RPA) availability to promote genomic stability. Nature Communications, 2021, 12, 5572.	5.8	11
105	New ammunition for the proteomic reactor: strong anion exchange beads and multiple enzymes enhance protein identification and sequence coverage. Analytical and Bioanalytical Chemistry, 2010, 397, 3421-3430.	1.9	10
106	Enhancing Membrane Protein Identification Using a Simplified Centrifugation and Detergent-Based Membrane Extraction Approach. Analytical Chemistry, 2018, 90, 2434-2439.	3.2	10
107	Quantitative proteomics reveals Shexiang Baoxin Pill exerts cardioprotective effects by preserving energy metabolism in a rat model of myocardial infarction. Journal of Ethnopharmacology, 2021, 266, 113460.	2.0	10
108	The Active Constituent From Gynostemma Pentaphyllum Prevents Liver Fibrosis Through Regulation of the TGF-β1/NDRG2/MAPK Axis. Frontiers in Genetics, 2020, 11, 594824.	1.1	9

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109	Identification of Highly Selective Lipoprotein-Associated Phospholipase A2 (Lp-PLA2) Inhibitors by a Covalent Fragment-Based Approach. Journal of Medicinal Chemistry, 2020, 63, 7052-7065.	2.9	8
110	Quantitative proteomic analysis uncovers inhibition of melanin synthesis by silk fibroin via MITF/tyrosinase axis in B16 melanoma cells. Life Sciences, 2021, 284, 119930.	2.0	8
111	Serum proteomic analysis reveals the cardioprotective effects of Shexiang Baoxin Pill and Suxiao Jiuxin Pill in a rat model of acute myocardial infarction. Journal of Ethnopharmacology, 2022, 293, 115279.	2.0	8
112	Establishment of a pseudovirus neutralization assay based on SARS-CoV-2 S protein incorporated into lentiviral particles. Biosafety and Health, 2022, 4, 38-44.	1.2	7
113	Deep Phosphoproteomic Measurements Pinpointing Drug Induced Protective Mechanisms in Neuronal Cells. Frontiers in Physiology, 2016, 7, 635.	1.3	6
114	The proteomic study of serially passaged human skin fibroblast cells uncovers down-regulation of the chromosome condensin complex proteins involved in replicative senescence. Biochemical and Biophysical Research Communications, 2018, 505, 1112-1120.	1.0	6
115	PGE2-JNK signaling axis non-canonically promotes Gli activation by protecting Gli2 from ubiquitin-proteasomal degradation. Cell Death and Disease, 2021, 12, 707.	2.7	6
116	Quantitative proteomic Analysis Reveals up-regulation of caveolin-1 in FOXP3-overexpressed human gastric cancer cells. Scientific Reports, 2017, 7, 14460.	1.6	5
117	Solution structure of extracellular loop of human β4 subunit of BK channel and its biological implication on ChTX sensitivity. Scientific Reports, 2018, 8, 4571.	1.6	5
118	Suppression of asparagine synthetase enhances the antitumor potency of ART and artemalogue SOMCL-14-221 in non-small cell lung cancer. Cancer Letters, 2020, 475, 22-33.	3.2	5
119	Label-free quantitative proteomic analysis identifies CTNNB1 as a direct target of FOXP3 in gastric cancer cells. Oncology Letters, 2018, 15, 7655-7660.	0.8	4
120	Uncovering kappa-opioid receptor agonist-induced PAK1/2 phosphorylation by quantitative phosphoproteomics. Biochemical and Biophysical Research Communications, 2019, 516, 320-326.	1.0	4
121	Targeting the RT loop of Src SH3 in Platelets Prevents Thrombosis without Compromising Hemostasis. Advanced Science, 2022, 9, e2103228.	5.6	4
122	Comparative Evaluation of Small Molecular Additives and Their Effects on Peptide/Protein Identification. Analytical Chemistry, 2017, 89, 5784-5792.	3.2	3
123	Revelation of AbfR in regulation of mismatch repair and energy metabolism in S. epidermidis by integrated proteomic and metabolomic analysis. Journal of Proteomics, 2020, 226, 103900.	1.2	2
124	MINING TANDEM MASS SPECTRAL DATA TO DEVELOP A MORE ACCURATE MASS ERROR MODEL FOR PEPTIDE IDENTIFICATION. , 2006, , .		2
125	A dataset resource for clinically associated phosphosites in hepatocellular carcinoma. Proteomics, 0, , 2100407.	1.3	2
126	Helix Matrix Transformation Combined With Convolutional Neural Network Algorithm for Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry-Based Bacterial Identification. Frontiers in Microbiology, 2020, 11, 565434.	1.5	1

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127	Recent advances in separation methods for post-translational modification proteomics. Chinese Journal of Chromatography (Se Pu), 2016, 34, 1199.	0.1	1
128	The quantitative proteomic analysis reveals schisantherin a prevents liver fibrosis through regulating extracellular matrix organization. International Journal of Mass Spectrometry, 2022, 480, 116898.	0.7	1