## Li-Rong Yu

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Distinct roles of GCN5/PCAF-mediated H3K9ac and CBP/p300-mediated H3K18/27ac in nuclear receptor transactivation. EMBO Journal, 2011, 30, 249-262.	7.8	655
2	Identification of JmjC domain-containing UTX and JMJD3 as histone H3 lysine 27 demethylases. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18439-18444.	7.1	607
3	Regulation of androgen receptor activity by tyrosine phosphorylation. Cancer Cell, 2006, 10, 309-319.	16.8	325
4	Self-Regulated Plk1 Recruitment to Kinetochores by the Plk1-PBIP1 Interaction Is Critical for Proper Chromosome Segregation. Molecular Cell, 2006, 24, 409-422.	9.7	235
5	Oxidant-induced apoptosis is mediated by oxidation of the actin-regulatory protein cofilin. Nature Cell Biology, 2009, 11, 1241-1246.	10.3	214
6	Transforming Growth Factor-β (TGF-β) Directly Activates the JAK1-STAT3 Axis to Induce Hepatic Fibrosis in Coordination with the SMAD Pathway. Journal of Biological Chemistry, 2017, 292, 4302-4312.	3.4	201
7	Identification of differentially expressed proteins between human hepatoma and normal liver cell lines by two-dimensional electrophoresis and liquidchromatography-ion trap mass spectrometry. Electrophoresis, 2000, 21, 3058-3068.	2.4	150
8	ldentification of a novel Wnt5a-CK1ε-Dvl2-Plk1-mediated primary cilia disassembly pathway. EMBO Journal, 2012, 31, 3104-3117.	7.8	148
9	Phosphoprotein Isotope-Coded Solid-Phase Tag Approach for Enrichment and Quantitative Analysis of Phosphopeptides from Complex Mixtures. Analytical Chemistry, 2003, 75, 5441-5450.	6.5	140
10	A detergent- and cyanogen bromide-free method for integral membrane proteomics: Application toHalobacterium purple membranes and the human epidermal membrane proteome. Proteomics, 2004, 4, 31-45.	2.2	140
11	CHD4 Has Oncogenic Functions in Initiating and Maintaining Epigenetic Suppression of Multiple Tumor Suppressor Genes. Cancer Cell, 2017, 31, 653-668.e7.	16.8	134
12	Improved Titanium Dioxide Enrichment of Phosphopeptides from HeLa Cells and High Confident Phosphopeptide Identification by Cross-Validation of MS/MS and MS/MS/MS Spectra. Journal of Proteome Research, 2007, 6, 4150-4162.	3.7	129
13	Polycyclic Aromatic Hydrocarbon Metabolic Network in Mycobacterium vanbaaleniiPYR-1. Journal of Bacteriology, 2011, 193, 4326-4337.	2.2	125
14	Coupling morphogenesis to mitotic entry. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 4124-4129.	7.1	116
15	A Combined Proteome and Microarray Investigation of Inorganic Phosphate-induced Pre-osteoblast Cells. Molecular and Cellular Proteomics, 2005, 4, 1284-1296.	3.8	113
16	Concerted mechanism of Swe1/Wee1 regulation by multiple kinases in budding yeast. EMBO Journal, 2005, 24, 2194-2204.	7.8	94
17	An integrated understanding of the physiological response to elevated extracellular phosphate. Journal of Cellular Physiology, 2013, 228, 1536-1550.	4.1	94
18	Multidimensional Proteome Analysis of Human Mammary Epithelial Cells. Journal of Proteome Research, 2004, 3, 68-75.	3.7	91

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19	Plk1-Dependent and -Independent Roles of an ODF2 Splice Variant, hCenexin1, at the Centrosome of Somatic Cells. Developmental Cell, 2009, 16, 539-550.	7.0	86
20	Regulation of microtubule-based microtubule nucleation by mammalian polo-like kinase 1. Proceedings of the United States of America, 2011, 108, 11446-11451.	7.1	86
21	Systematic Proteome Analysis Identifies Transcription Factor YY1 as a Direct Target of miR-34a. Journal of Proteome Research, 2011, 10, 479-487.	3.7	84
22	Proteomic analysis of detergent-resistant membrane rafts. Electrophoresis, 2004, 25, 1307-1318.	2.4	78
23	A Proteomic Characterization of the Plasma Membrane of Human Epidermis by High-Throughput Mass Spectrometry. Journal of Investigative Dermatology, 2004, 123, 691-699.	0.7	76
24	Quantitative Profiling of the Detergent-Resistant Membrane Proteome of Iota-b Toxin Induced Vero Cells. Journal of Proteome Research, 2005, 4, 523-531.	3.7	75
25	A Negative Feedback Control of Transforming Growth Factor-Î <sup>2</sup> Signaling by Glycogen Synthase Kinase 3-mediated Smad3 Linker Phosphorylation at Ser-204. Journal of Biological Chemistry, 2009, 284, 19808-19816.	3.4	69
26	Evaluation of the Acid-Cleavable Isotope-Coded Affinity Tag Reagents:Â Application to Camptothecin-Treated Cortical Neurons. Journal of Proteome Research, 2004, 3, 469-477.	3.7	64
27	RSK-Mediated Phosphorylation in the C/EBPÎ <sup>2</sup> Leucine Zipper Regulates DNA Binding, Dimerization, and Growth Arrest Activity. Molecular and Cellular Biology, 2010, 30, 2621-2635.	2.3	63
28	On-Column Sample Enrichment for Capillary Electrophoresis Sheathless Electrospray Ionization Mass Spectrometry:Â Evaluation for Peptide Analysis and Protein Identification. Analytical Chemistry, 2003, 75, 5984-5993.	6.5	61
29	Global Analysis of the Cortical Neuron Proteome. Molecular and Cellular Proteomics, 2004, 3, 896-907.	3.8	58
30	Apoptosis of enterocytes and nitration of junctional complex proteins promote alcohol-induced gut leakiness and liver injury. Journal of Hepatology, 2018, 69, 142-153.	3.7	58
31	MicroRNA hsa-miR-370-3p suppresses the expression and induction of CYP2D6 by facilitating mRNA degradation. Biochemical Pharmacology, 2017, 140, 139-149.	4.4	57
32	Proteins in aggregates functionally impact multiple neurodegenerative disease models by forming proteasomeâ€blocking complexes. Aging Cell, 2015, 14, 35-48.	6.7	54
33	Mechanism of 3,4â€methylenedioxymethamphetamine (MDMA, ecstasy)â€mediated mitochondrial dysfunction in rat liver. Proteomics, 2008, 8, 3906-3918.	2.2	53
34	Combined Chemical and Enzymatic Stable Isotope Labeling for Quantitative Profiling of Detergent-Insoluble Membrane Proteins Isolated Using Triton X-100 and Brij-96. Journal of Proteome Research, 2006, 5, 349-360.	3.7	52
35	Direct Phosphorylation and Activation of a Nim1-related Kinase Gin4 by Elm1 in Budding Yeast. Journal of Biological Chemistry, 2006, 281, 27090-27098.	3.4	51
36	Quantitative proteomic analysis of inorganic phosphate-induced murine MC3T3-E1 osteoblast cells. Electrophoresis, 2004, 25, 1342-1352.	2.4	45

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37	Phosphoproteomics for the discovery of kinases as cancer biomarkers and drug targets. Proteomics - Clinical Applications, 2007, 1, 1042-1057.	1.6	42
38	Critical role of c-jun N-terminal protein kinase in promoting mitochondrial dysfunction and acute liver injury. Redox Biology, 2015, 6, 552-564.	9.0	41
39	Global Genomic and Proteomic Analysis Identifies Biological Pathways Related to High-Risk Neuroblastoma. Journal of Proteome Research, 2010, 9, 373-382.	3.7	38
40	Proteome analysis of camptothecin-treated cortical neurons using isotope-coded affinity tags. Electrophoresis, 2002, 23, 1591.	2.4	37
41	Proteomic analysis of early response lymph node proteins in mice treated with titanium dioxide nanoparticles. Journal of Proteomics, 2011, 74, 2745-2759.	2.4	37
42	Early metabolomics changes in heart and plasma during chronic doxorubicin treatment in B6C3F <sub>1</sub> mice. Journal of Applied Toxicology, 2016, 36, 1486-1495.	2.8	37
43	Functional Robustness of a Polycyclic Aromatic Hydrocarbon Metabolic Network Examined in a <i>nidA</i> Aromatic Ring-Hydroxylating Oxygenase Mutant of Mycobacterium vanbaalenii PYR-1. Applied and Environmental Microbiology, 2012, 78, 3715-3723.	3.1	36
44	A systematic evaluation of microRNAs in regulating human hepatic CYP2E1. Biochemical Pharmacology, 2017, 138, 174-184.	4.4	36
45	Requirement for the Budding Yeast Polo Kinase Cdc5 in Proper Microtubule Growth and Dynamics. Eukaryotic Cell, 2008, 7, 444-453.	3.4	35
46	Early transcriptional changes in cardiac mitochondria during chronic doxorubicin exposure and mitigation by dexrazoxane in mice. Toxicology and Applied Pharmacology, 2016, 295, 68-84.	2.8	33
47	Integrated microRNA, mRNA, and protein expression profiling reveals microRNA regulatory networks in rat kidney treated with a carcinogenic dose of aristolochic acid. BMC Genomics, 2015, 16, 365.	2.8	32
48	The Proteomics of Neurodegeneration. Molecular Diagnosis and Therapy, 2005, 5, 259-270.	3.3	30
49	Quantitative proteomics for drug toxicity. Briefings in Functional Genomics & Proteomics, 2009, 8, 158-166.	3.8	29
50	Immune response proteins as predictive biomarkers of doxorubicin-induced cardiotoxicity in breast cancer patients. Experimental Biology and Medicine, 2018, 243, 248-255.	2.4	29
51	Proteome alterations in human hepatoma cells transfected with antisense epidermal growth factor receptor sequence. Electrophoresis, 2001, 22, 3001-3008.	2.4	28
52	Detection ofin situ labeled cell surface proteins by mass spectrometry: Application to the membrane subproteome of human mammary epithelial cells. Proteomics, 2003, 3, 1647-1651.	2.2	27
53	Proteomic analysis of acetaminophen-induced hepatotoxicity and identification of heme oxygenase 1 as a potential plasma biomarker of liver injury. Proteomics - Clinical Applications, 2017, 11, 1600123.	1.6	26
54	Proteome Analysis of DNA Damage-induced Neuronal Death Using High Throughput Mass Spectrometry. Journal of Biological Chemistry, 2004, 279, 26685-26697.	3.4	25

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55	Aptamer-Based Proteomics Identifies Mortality-Associated Serum Biomarkers in Dialysis-Dependent AKI Patients. Kidney International Reports, 2018, 3, 1202-1213.	0.8	20
56	An Integrated Analysis of Metabolites, Peptides, and Inflammation Biomarkers for Assessment of Preanalytical Variability of Human Plasma. Journal of Proteome Research, 2019, 18, 2411-2421.	3.7	20
57	Analysis of Murine Natural Killer Cell Microsomal Proteins Using Two-Dimensional Liquid Chromatography Coupled to Tandem Electrospray Ionization Mass Spectrometry. Journal of Proteome Research, 2004, 3, 862-870.	3.7	19
58	Pharmacoproteomics and toxicoproteomics: The field of dreams. Journal of Proteomics, 2011, 74, 2549-2553.	2.4	18
59	Stability of the Human Plasma Proteome to Pre-analytical Variability as Assessed by an Aptamer-Based Approach. Journal of Proteome Research, 2019, 18, 3661-3670.	3.7	17
60	Increased oxidativeâ€modifications of cytosolic proteins in 3,4â€methylenedioxymethamphetamine (MDMA,) Tj	ет <u>9</u> 0000	rgBT /Overlo
61	Inhibition of Staphylococcus aureus by Lysostaphin-Expressing Lactobacillus plantarum WCFS1 in a Modified Genital Tract Secretion Medium. Applied and Environmental Microbiology, 2011, 77, 8500-8508.	3.1	16
62	Discovery of Novel Proteomic Biomarkers for the Prediction of Kidney Recovery from Dialysis-Dependent AKI Patients. Kidney360, 2021, 2, 1716-1727.	2.1	16
63	Profiling the activity of G proteins in patient-derived tissues by rapid affinity-capture of signal transduction proteins (GRASP). Proteomics, 2004, 4, 812-818.	2.2	14
64	Quantitative Proteomic Analysis of Sokotrasterol Sulfate-stimulated Primary Human Endothelial Cells. Molecular and Cellular Proteomics, 2005, 4, 191-204.	3.8	14
65	Identification of the Enzyme Responsible for <i>N</i> -Acetylation of Norfloxacin by Microbacterium sp. Strain 4N2-2. Applied and Environmental Microbiology, 2013, 79, 314-321.	3.1	14
66	Proteomics quality and standard: From a regulatory perspective. Journal of Proteomics, 2014, 96, 353-359.	2.4	11
67	Pooled ORF Expression Technology (POET). Molecular and Cellular Proteomics, 2005, 4, 1647-1652.	3.8	10
68	Proteomic Analysis by Two-Dimensional Polyacrylamide Gel Electrophoresis. Advances in Protein Chemistry, 2003, 65, 57-84.	4.4	9
69	Parallel Analysis of Transcript and Translation Profiles:Â Identification of Metastasis-Related Signal Pathways Differentially Regulated by Drug and Genetic Modifications. Journal of Proteome Research, 2006, 5, 1555-1567.	3.7	9
70	Quantitative proteomic analysis of human breast epithelial cells with differential telomere length. Biochemical and Biophysical Research Communications, 2007, 356, 942-947.	2.1	9
71	Serum metabolite profiles predict outcomes in critically ill patients receiving renal replacement therapy. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2021, 1187, 123024.	2.3	8
72	Diagnostic Proteomics: Serum Proteomic Patterns for the Detection of Early Stage Cancers. Disease Markers, 2004, 19, 209-218.	1.3	7

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73	Phosphopeptide Enrichment Using Offline Titanium Dioxide Columns for Phosphoproteomics. Methods in Molecular Biology, 2013, 1002, 93-103.	0.9	7
74	Cell cycle-dependent phosphorylation of nucleophosmin and its potential regulation by peptidyl-prolyl cis/trans isomerase. Journal of Molecular Biochemistry, 2015, 4, 95-103.	0.1	7
75	AACR–FDA–NCI cancer biomarkers collaborative. Expert Review of Molecular Diagnostics, 2007, 7, 507-509.	3.1	4
76	Characterization of Phosphorylated Proteins Using Mass Spectrometry. Current Protein and Peptide Science, 2021, 22, 148-157.	1.4	4
77	Mass Spectrometry–Based Proteomics for Biomarker Discovery. Methods in Molecular Biology, 2022, 2486, 3-17.	0.9	4
78	Proteomic analysis of protein expression changes in a model of gliomagenesis. Proteomics - Clinical Applications, 2007, 1, 1485-1498.	1.6	3
79	Doxorubicin Cardiotoxicity: Preclinical and Clinical Circulating Protein Markers. Biomarkers in Disease, 2022, , 1-27.	0.1	1
80	Proteomics: The Deciphering of the Functional Genome. , 2009, , 173-179.		0
81	An Aptamerâ€Based Approach to Assess the Human Plasma Proteome for Preâ€Analytical Variability. FASEB Journal, 2018, 32, 802.5.	0.5	0