

# Yansheng Liu

## List of Publications by Year in descending order

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57  
papers

7,262  
citations

172457

29  
h-index

149698

56  
g-index

73  
all docs

73  
docs citations

73  
times ranked

12533  
citing authors

#	ARTICLE	IF	CITATIONS
1	On the Dependency of Cellular Protein Levels on mRNA Abundance. <i>Cell</i> , 2016, 165, 535-550.	28.9	2,216
2	Integrated Proteogenomic Characterization of HBV-Related Hepatocellular Carcinoma. <i>Cell</i> , 2019, 179, 561-577.e22.	28.9	629
3	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017, 8, 291.	12.8	423
4	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031.	5.3	370
5	Quantitative variability of 342 plasma proteins in a human twin population. <i>Molecular Systems Biology</i> , 2015, 11, 786.	7.2	300
6	Multi-omic measurements of heterogeneity in HeLa cells across laboratories. <i>Nature Biotechnology</i> , 2019, 37, 314-322.	17.5	254
7	Protein kinase D at the Golgi controls NLRP3 inflammasome activation. <i>Journal of Experimental Medicine</i> , 2017, 214, 2671-2693.	8.5	197
8	Quantitative measurements of N-linked glycoproteins in human plasma by SWATH-MS. <i>Proteomics</i> , 2013, 13, 1247-1256.	2.2	190
9	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. <i>Nature Methods</i> , 2017, 14, 921-927.	19.0	189
10	Using data-independent, high-resolution mass spectrometry in protein biomarker research: Perspectives and clinical applications. <i>Proteomics - Clinical Applications</i> , 2015, 9, 307-321.	1.6	182
11	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. <i>Nature Methods</i> , 2016, 13, 777-783.	19.0	173
12	Glycoproteomic Analysis of Prostate Cancer Tissues by SWATH Mass Spectrometry Discovers N-acyl ethanolamine Acid Amidase and Protein Tyrosine Kinase 7 as Signatures for Tumor Aggressiveness. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1753-1768.	3.8	165
13	A Class of Environmental and Endogenous Toxins Induces BRCA2 Haploinsufficiency and Genome Instability. <i>Cell</i> , 2017, 169, 1105-1118.e15.	28.9	149
14	Impact of Alternative Splicing on the Human Proteome. <i>Cell Reports</i> , 2017, 20, 1229-1241.	6.4	145
15	Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , 2017, 35, 781-788.	17.5	122
16	Mass spectrometric protein maps for biomarker discovery and clinical research. <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 811-825.	3.1	117
17	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. <i>Nature Communications</i> , 2017, 8, 1212.	12.8	112
18	Prediction of colorectal cancer diagnosis based on circulating plasma proteins. <i>EMBO Molecular Medicine</i> , 2015, 7, 1166-1178.	6.9	80

#	ARTICLE	IF	CITATIONS
19	NAguideR: performing and prioritizing missing value imputations for consistent bottom-up proteomic analyses. <i>Nucleic Acids Research</i> , 2020, 48, e83-e83.	14.5	77
20	Strategies to enable large-scale proteomics for reproducible research. <i>Nature Communications</i> , 2020, 11, 3793.	12.8	75
21	Breast Cancer Classification Based on Proteotypes Obtained by SWATH Mass Spectrometry. <i>Cell Reports</i> , 2019, 28, 832-843.e7.	6.4	72
22	Integrative Proteomics and Tissue Microarray Profiling Indicate the Association between Overexpressed Serum Proteins and Non-Small Cell Lung Cancer. <i>PLoS ONE</i> , 2012, 7, e51748.	2.5	58
23	Global and Site-Specific Effect of Phosphorylation on Protein Turnover. <i>Developmental Cell</i> , 2021, 56, 111-124.e6.	7.0	57
24	A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. <i>Cell Systems</i> , 2020, 10, 133-155.e6.	6.2	57
25	Isoform-resolved correlation analysis between mRNA abundance regulation and protein level degradation. <i>Molecular Systems Biology</i> , 2020, 16, e9170.	7.2	42
26	A high-quality secretome of A549 cells aided the discovery of C4b-binding protein as a novel serum biomarker for non-small cell lung cancer. <i>Journal of Proteomics</i> , 2011, 74, 528-538.	2.4	38
27	Speeding up tandem mass spectrometry based database searching by peptide and spectrum indexing. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 807-814.	1.5	37
28	Similarities and Differences of Blood N-Glycoproteins in Five Solid Carcinomas at Localized Clinical Stage Analyzed by SWATH-MS. <i>Cell Reports</i> , 2018, 23, 2819-2831.e5.	6.4	36
29	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. <i>Nature Communications</i> , 2019, 10, 2524.	12.8	35
30	Multiplexed Targeted Mass Spectrometry-Based Assays for the Quantification of N-Linked Glycosite-Containing Peptides in Serum. <i>Analytical Chemistry</i> , 2015, 87, 10830-10838.	6.5	32
31	Combining Rapid Data Independent Acquisition and CRISPR Gene Deletion for Studying Potential Protein Functions: A Case of HMG1. <i>Proteomics</i> , 2019, 19, e1800438.	2.2	31
32	Quantitative Proteomics Reveal up-regulated Protein Expression of the SET Complex Associated with Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2012, 11, 871-885.	3.7	30
33	Assessing the Relationship Between Mass Window Width and Retention Time Scheduling on Protein Coverage for Data-Independent Acquisition. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1396-1405.	2.8	30
34	Shotgun and targeted proteomics reveal that pre-surgery serum levels of LRG1, SAA, and C4BP may refine prognosis of resected squamous cell lung cancer. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 344-347.	3.3	28
35	Image-based computational quantification and visualization of genetic alterations and tumour heterogeneity. <i>Scientific Reports</i> , 2016, 6, 24146.	3.3	28
36	The interdependence of transcript and protein abundance: new data—new complexities. <i>Molecular Systems Biology</i> , 2016, 12, 856.	7.2	26

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37	SECAT: Quantifying Protein Complex Dynamics across Cell States by Network-Centric Analysis of SEC-SWATH-MS Profiles. <i>Cell Systems</i> , 2020, 11, 589-607.e8.	6.2	26
38	Germ-free and microbiota-associated mice yield small intestinal epithelial organoids with equivalent and robust transcriptome/proteome expression phenotypes. <i>Cellular Microbiology</i> , 2020, 22, e13191.	2.1	26
39	Data-independent acquisition-based proteome and phosphoproteome profiling across six melanoma cell lines reveals determinants of proteotypes. <i>Molecular Omics</i> , 2021, 17, 413-425.	2.8	26
40	motifer: An Integrated Web Software for Identification and Visualization of Protein Posttranslational Modification Motifs. <i>Proteomics</i> , 2019, 19, e1900245.	2.2	25
41	Selection of Features with Consistent Profiles Improves Relative Protein Quantification in Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 944-959.	3.8	25
42	BoxCarMax: A High-Selectivity Data-Independent Acquisition Mass Spectrometry Method for the Analysis of Protein Turnover and Complex Samples. <i>Analytical Chemistry</i> , 2021, 93, 3103-3111.	6.5	24
43	Proteomic mining in the dysplastic liver of WHV/cmyc mice – insights and indicators for early hepatocarcinogenesis. <i>FEBS Journal</i> , 2010, 277, 4039-4053.	4.7	23
44	Comparison of targeted proteomics approaches for detecting and quantifying proteins derived from human cancer tissues. <i>Proteomics</i> , 2017, 17, 1600323.	2.2	22
45	Cross-compartment signal propagation in the mitotic exit network. <i>ELife</i> , 2021, 10, .	6.0	21
46	FGF23 contains two distinct high-affinity binding sites enabling bivalent interactions with Klotho. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31800-31807.	7.1	18
47	A PKD-MFF signaling axis couples mitochondrial fission to mitotic progression. <i>Cell Reports</i> , 2021, 35, 109129.	6.4	15
48	Capillary zone electrophoresis-tandem mass spectrometry with ultraviolet photodissociation (213 nm) for large-scale top-down proteomics. <i>Analytical Methods</i> , 2019, 11, 2855-2861.	2.7	14
49	Systems pharmacology using mass spectrometry identifies critical response nodes in prostate cancer. <i>Npj Systems Biology and Applications</i> , 2018, 4, 26.	3.0	13
50	MAL2 mediates the formation of stable HER2 signaling complexes within lipid raft-rich membrane protrusions in breast cancer cells. <i>Cell Reports</i> , 2021, 37, 110160.	6.4	12
51	A peptidome based proteomic strategy for studying functions of post-translational modifications. <i>Proteomics</i> , 2022, 22, 2100316.	2.2	7
52	Deep Phosphoproteomic Measurements Pinpointing Drug Induced Protective Mechanisms in Neuronal Cells. <i>Frontiers in Physiology</i> , 2016, 7, 635.	2.8	6
53	Multi-in-One: Multiple-Proteases, One-Hour-Shot Strategy for Fast and High-Coverage Phosphoproteomic Investigation. <i>Analytical Chemistry</i> , 2020, 92, 8943-8951.	6.5	6
54	Developing a Bimolecular Affinity Purification Strategy to Isolate 26S Proteasome Holocomplexes for Complex-Centric Proteomic Analysis. <i>Analytical Chemistry</i> , 2021, 93, 13407-13413.	6.5	5

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55	Statistical elimination of spectral features with large between-run variation enhances quantitative protein-level conclusions in experiments with data-independent spectral acquisition. BMC Bioinformatics, 2015, 16, .	2.6	1
56	Respective, Timeâ€-dependent Phosphorylation Modules Shaping Phosphoproteome Abundance and Turnover. FASEB Journal, 2021, 35, .	0.5	0
57	Identification and Characterization of Epigenetic Regulators of Breast Cancer Metastasis to the Brain. FASEB Journal, 2021, 35, .	0.5	0