

# Yingwei hu

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

2,591  
citations

257429

24  
h-index

243610

44  
g-index

50  
all docs

50  
docs citations

50  
times ranked

3460  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of <i>In Vivo</i> Protein Complexes via Chemical Cross-Linking and Mass Spectrometry. <i>Analytical Chemistry</i> , 2022, 94, 1537-1542.	6.5	3
2	Improving the detection of aggressive prostate cancer using immunohistochemical staining of protein marker panels.. <i>American Journal of Cancer Research</i> , 2022, 12, 1323-1336.	1.4	0
3	Characterization of core fucosylation via sequential enzymatic treatments of intact glycopeptides and mass spectrometry analysis. <i>Nature Communications</i> , 2022, 13, .	12.8	14
4	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	16.8	189
5	Proteomics Landscape of Host-Pathogen Interaction in <i>Acinetobacter baumannii</i> Infected Mouse Lung. <i>Frontiers in Genetics</i> , 2021, 12, 563516.	2.3	2
6	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	28.9	236
7	Proteomic characterization of primary and metastatic prostate cancer reveals reduced proteinase activity in aggressive tumors. <i>Scientific Reports</i> , 2021, 11, 18936.	3.3	6
8	Data-Independent Acquisition-Based Mass Spectrometry (DIA-MS) for Quantitative Analysis of Intact N-Linked Glycopeptides. <i>Analytical Chemistry</i> , 2021, 93, 13774-13782.	6.5	14
9	Community evaluation of glycoproteomics informatics solutions reveals high-performance search strategies for serum glycopeptide analysis. <i>Nature Methods</i> , 2021, 18, 1304-1316.	19.0	74
10	Abstract IA-003: Proteogenomic characterizations of pancreatic ductal adenocarcinoma. , 2021, , .		0
11	OmicsOne: associate omics data with phenotypes in one-click. <i>Clinical Proteomics</i> , 2021, 18, 29.	2.1	2
12	Glycoproteomics-based signatures for tumor subtyping and clinical outcome prediction of high-grade serous ovarian cancer. <i>Nature Communications</i> , 2020, 11, 6139.	12.8	72
13	Comparison of Three Glycoproteomic Methods for the Analysis of the Secretome of CHO Cells Treated with 1,3,4-O-Bu3ManNAc. <i>Bioengineering</i> , 2020, 7, 144.	3.5	4
14	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020, 33, 108276.	6.4	83
15	Proteomic signatures of 16 major types of human cancer reveal universal and cancer-type-specific proteins for the identification of potential therapeutic targets. <i>Journal of Hematology and Oncology</i> , 2020, 13, 170.	17.0	25
16	Impact of Increased FUT8 Expression on the Extracellular Vesicle Proteome in Prostate Cancer Cells. <i>Journal of Proteome Research</i> , 2020, 19, 2195-2205.	3.7	28
17	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
18	N-GlycositeAtlas: a database resource for mass spectrometry-based human N-linked glycoprotein and glycosylation site mapping. <i>Clinical Proteomics</i> , 2019, 16, 35.	2.1	56

#	ARTICLE	IF	CITATIONS
19	Deciphering the Roles of N-Glycans on Collagenâ€“Platelet Interactions. <i>Journal of Proteome Research</i> , 2019, 18, 2467-2477.	3.7	14
20	Simple Tip-Based Sample Processing Method for Urinary Proteomic Analysis. <i>Analytical Chemistry</i> , 2019, 91, 5517-5522.	6.5	18
21	Mapping human N-linked glycoproteins and glycosylation sites using mass spectrometry. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 114, 143-150.	11.4	27
22	Combining Butyrate ManNAc with Glycoengineered CHO Cells Improves EPO Glycan Quality and Production. <i>Biotechnology Journal</i> , 2019, 14, 1800186.	3.5	23
23	Intact Glycopeptide Analysis of Influenza A/H1N1/09 Neuraminidase Revealing the Effects of Host and Glycosite Location on Siteâ€“Specific Glycan Structures. <i>Proteomics</i> , 2019, 19, 1800202.	2.2	5
24	Developing Workflow for Simultaneous Analyses of Phosphopeptides and Glycopeptides. <i>ACS Chemical Biology</i> , 2019, 14, 58-66.	3.4	31
25	Site-Specific Profiling of Serum Glycoproteins Using N-Linked Glycan and Glycosite Analysis Revealing Atypical N-Glycosylation Sites on Albumin and Î±1B-Glycoprotein. <i>Analytical Chemistry</i> , 2018, 90, 6292-6299.	6.5	44
26	Overexpression of Î± (1,6) fucosyltransferase in the development of castration-resistant prostate cancer cells. <i>Prostate Cancer and Prostatic Diseases</i> , 2018, 21, 137-146.	3.9	35
27	Evaluation of NCI-7 Cell Line Panel as a Reference Material for Clinical Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2205-2215.	3.7	17
28	Mapping the Oâ€“glycoproteome using siteâ€“specific extraction of Oâ€“linked glycopeptides (EXoO). <i>Molecular Systems Biology</i> , 2018, 14, e8486.	7.2	110
29	Comprehensive Glycoproteomic Analysis of Chinese Hamster Ovary Cells. <i>Analytical Chemistry</i> , 2018, 90, 14294-14302.	6.5	42
30	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatographyâ€“mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 1632-1661.	12.0	377
31	Reanalysis of Global Proteomic and Phosphoproteomic Data Identified a Large Number of Glycopeptides. <i>Analytical Chemistry</i> , 2018, 90, 8065-8071.	6.5	81
32	Proteomics analyses of prostate cancer cells reveal cellular pathways associated with androgen resistance. <i>Proteomics</i> , 2017, 17, 1600228.	2.2	18
33	Modification of Sialic Acids on Solid Phase: Accurate Characterization of Protein Sialylation. <i>Analytical Chemistry</i> , 2017, 89, 6330-6335.	6.5	39
34	Simultaneous quantification of N- and O-glycans using a solid-phase method. <i>Nature Protocols</i> , 2017, 12, 1229-1244.	12.0	57
35	Site-Specific Fucosylation Analysis Identifying Glycoproteins Associated with Aggressive Prostate Cancer Cell Lines Using Tandem Affinity Enrichments of Intact Glycopeptides Followed by Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 7623-7630.	6.5	65
36	Comparison of Enrichment Methods for Intact N- and O-Linked Glycopeptides Using Strong Anion Exchange and Hydrophilic Interaction Liquid Chromatography. <i>Analytical Chemistry</i> , 2017, 89, 11193-11197.	6.5	93

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37	Overexpression of Exportin-5 Overrides the Inhibitory Effect of miRNAs Regulation Control and Stabilize Proteins via Posttranslation Modifications in Prostate Cancer. <i>Neoplasia</i> , 2017, 19, 817-829.	5.3	8
38	An integrated proteomic and glycoproteomic approach uncovers differences in glycosylation occupancy from benign and malignant epithelial ovarian tumors. <i>Clinical Proteomics</i> , 2017, 14, 16.	2.1	14
39	Classification of Tandem Mass Spectra for Identification of N- and O-linked Glycopeptides. <i>Scientific Reports</i> , 2016, 6, 37189.	3.3	45
40	Direct glycan structure determination of intact N-linked glycopeptides by low-energy collision-induced dissociation tandem mass spectrometry and predicted spectral library searching. <i>Analytica Chimica Acta</i> , 2016, 934, 152-162.	5.4	21
41	Proteomic response of methicillin-resistant <i>S. aureus</i> to a synergistic antibacterial drug combination: a novel erythromycin derivative and oxacillin. <i>Scientific Reports</i> , 2016, 6, 19841.	3.3	29
42	Label-Free Quantitative Proteomics Analysis of Antibiotic Response in <i>Staphylococcus aureus</i> to Oxacillin. <i>Journal of Proteome Research</i> , 2014, 13, 1223-1233.	3.7	71
43	A High-Resolution LC-MS-Based Secondary Metabolite Fingerprint Database of Marine Bacteria. <i>Scientific Reports</i> , 2014, 4, 6537.	3.3	17
44	Expanding Tandem Mass Spectral Libraries of Phosphorylated Peptides: Advances and Applications. <i>Journal of Proteome Research</i> , 2013, 12, 5971-5977.	3.7	21
45	A semi-empirical approach for predicting unobserved peptide MS/MS spectra from spectral libraries. <i>Proteomics</i> , 2011, 11, 4702-4711.	2.2	17