

# Fuchu He

## List of Publications by Year in descending order

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97  
papers

8,980  
citations

76326

40  
h-index

43889

91  
g-index

98  
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98  
docs citations

98  
times ranked

14552  
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulation of Cellular Metabolism by Protein Lysine Acetylation. <i>Science</i> , 2010, 327, 1000-1004.	12.6	1,642
2	iProX: an integrated proteome resource. <i>Nucleic Acids Research</i> , 2019, 47, D1211-D1217.	14.5	1,001
3	Proteomics identifies new therapeutic targets of early-stage hepatocellular carcinoma. <i>Nature</i> , 2019, 567, 257-261.	27.8	613
4	A genome-wide association study of nasopharyngeal carcinoma identifies three new susceptibility loci. <i>Nature Genetics</i> , 2010, 42, 599-603.	21.4	374
5	Genome-wide association study identifies 1p36.22 as a new susceptibility locus for hepatocellular carcinoma in chronic hepatitis B virus carriers. <i>Nature Genetics</i> , 2010, 42, 755-758.	21.4	319
6	Integrative Proteomic Characterization of Human Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 245-261.e17.	28.9	300
7	LSECTin Expressed on Melanoma Cells Promotes Tumor Progression by Inhibiting Antitumor T-cell Responses. <i>Cancer Research</i> , 2014, 74, 3418-3428.	0.9	270
8	Neutrophils promote the development of reparative macrophages mediated by ROS to orchestrate liver repair. <i>Nature Communications</i> , 2019, 10, 1076.	12.8	231
9	iProX in 2021: connecting proteomics data sharing with big data. <i>Nucleic Acids Research</i> , 2022, 50, D1522-D1527.	14.5	197
10	Toward an understanding of the protein interaction network of the human liver. <i>Molecular Systems Biology</i> , 2011, 7, 536.	7.2	194
11	A proteomic landscape of diffuse-type gastric cancer. <i>Nature Communications</i> , 2018, 9, 1012.	12.8	175
12	Targeting WW domains linker of HECT-type ubiquitin ligase Smurf1 for activation by CKIP-1. <i>Nature Cell Biology</i> , 2008, 10, 994-1002.	10.3	159
13	The covalent modifier Nedd8 is critical for the activation of Smurf1 ubiquitin ligase in tumorigenesis. <i>Nature Communications</i> , 2014, 5, 3733.	12.8	157
14	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155
15	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301.	12.8	152
16	An integrated bioinformatics platform for investigating the human E3 ubiquitin ligase-substrate interaction network. <i>Nature Communications</i> , 2017, 8, 347.	12.8	151
17	Deubiquitylase OTUD3 regulates PTEN stability and suppresses tumorigenesis. <i>Nature Cell Biology</i> , 2015, 17, 1169-1181.	10.3	135
18	Association between Mannose-Binding Lectin Gene Polymorphisms and Susceptibility to Severe Acute Respiratory Syndrome Coronavirus Infection. <i>Journal of Infectious Diseases</i> , 2005, 192, 1355-1361.	4.0	125

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19	A proteomics landscape of circadian clock in mouse liver. <i>Nature Communications</i> , 2018, 9, 1553.	12.8	115
20	Long Noncoding RNA p53 <sup>ΔE</sup> Stabilizing and Activating RNA Promotes p53 Signaling by Inhibiting Heterogeneous Nuclear Ribonucleoprotein K deSUMOylation and Suppresses Hepatocellular Carcinoma. <i>Hepatology</i> , 2020, 71, 112-129.	7.3	104
21	Comprehensive Proteomics Analysis Reveals Metabolic Reprogramming of Tumor-Associated Macrophages Stimulated by the Tumor Microenvironment. <i>Journal of Proteome Research</i> , 2017, 16, 288-297.	3.7	95
22	A Fast Workflow for Identification and Quantification of Proteomes. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2370-2380.	3.8	94
23	A Cell-type-resolved Liver Proteome. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3190-3202.	3.8	83
24	Functional polymorphisms of the CCL2 and MBL genes cumulatively increase susceptibility to severe acute respiratory syndrome coronavirus infection. <i>Journal of Infection</i> , 2015, 71, 101-109.	3.3	78
25	Mutually exclusive acetylation and ubiquitylation of the splicing factor SRSF5 control tumor growth. <i>Nature Communications</i> , 2018, 9, 2464.	12.8	77
26	Germline Duplication of SNORA18L5 Increases Risk for HBV-related Hepatocellular Carcinoma by Altering Localization of Ribosomal Proteins and Decreasing Levels of p53. <i>Gastroenterology</i> , 2018, 155, 542-556.	1.3	75
27	Estrogen Receptor $\beta$ Polymorphisms Associated With Susceptibility to Hepatocellular Carcinoma in Hepatitis B Virus Carriers. <i>Gastroenterology</i> , 2006, 130, 2001-2009.	1.3	74
28	CKIP-1 Inhibits Cardiac Hypertrophy by Regulating Class II Histone Deacetylase Phosphorylation Through Recruiting PP2A. <i>Circulation</i> , 2012, 126, 3028-3040.	1.6	72
29	Role for the pleckstrin homology domain-containing protein CKIP-1 in AP-1 regulation and apoptosis. <i>EMBO Journal</i> , 2005, 24, 766-778.	7.8	70
30	Human Liver Proteome Project. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1841-1848.	3.8	67
31	Smad Ubiquitylation Regulatory Factor 1/2 (Smurf1/2) Promotes p53 Degradation by Stabilizing the E3 Ligase MDM2. <i>Journal of Biological Chemistry</i> , 2010, 285, 22818-22830.	3.4	67
32	CKIP-1 regulates macrophage proliferation by inhibiting TRAF6-mediated Akt activation. <i>Cell Research</i> , 2014, 24, 742-761.	12.0	67
33	Dysregulated Response of Follicular Helper T Cells to Hepatitis B Surface Antigen Promotes HBV Persistence in Mice and Associates With Outcomes of Patients. <i>Gastroenterology</i> , 2018, 154, 2222-2236.	1.3	67
34	Neddylation of PTEN regulates its nuclear import and promotes tumor development. <i>Cell Research</i> , 2021, 31, 291-311.	12.0	67
35	The E3 Ligase Smurf1 Regulates Wolfram Syndrome Protein Stability at the Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2011, 286, 18037-18047.	3.4	62
36	Genome-wide association study identifies 8p21.3 associated with persistent hepatitis B virus infection among Chinese. <i>Nature Communications</i> , 2016, 7, 11664.	12.8	54

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37	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3415-3431.	3.7	53
38	Histone H3K27 methyltransferase EZH2 and demethylase JMJD3 regulate hepatic stellate cells activation and liver fibrosis. <i>Theranostics</i> , 2021, 11, 361-378.	10.0	48
39	The Ubiquitin Ligase TRAF6 Negatively Regulates the JAK-STAT Signaling Pathway by Binding to STAT3 and Mediating Its Ubiquitination. <i>PLoS ONE</i> , 2012, 7, e49567.	2.5	48
40	Dynamic ubiquitylation of Sox2 regulates proteostasis and governs neural progenitor cell differentiation. <i>Nature Communications</i> , 2018, 9, 4648.	12.8	47
41	UbiBrowser 2.0: a comprehensive resource for proteome-wide known and predicted ubiquitin ligase/deubiquitinase substrate interactions in eukaryotic species. <i>Nucleic Acids Research</i> , 2022, 50, D719-D728.	14.5	46
42	An extended genome-wide association study identifies novel susceptibility loci for nasopharyngeal carcinoma. <i>Human Molecular Genetics</i> , 2016, 25, 3626-3634.	2.9	42
43	ER-associated ubiquitin ligase HRD1 programs liver metabolism by targeting multiple metabolic enzymes. <i>Nature Communications</i> , 2018, 9, 3659.	12.8	42
44	CKIP-1 limits foam cell formation and inhibits atherosclerosis by promoting degradation of Oct-1 by REG1 $\beta$ . <i>Nature Communications</i> , 2019, 10, 425.	12.8	42
45	Histone H3K9 demethylase JMJD1A modulates hepatic stellate cells activation and liver fibrosis by epigenetically regulating peroxisome proliferator-activated receptor $\beta$ . <i>FASEB Journal</i> , 2015, 29, 1830-1841.	0.5	41
46	Genome-wide association study of COVID-19 severity among the Chinese population. <i>Cell Discovery</i> , 2021, 7, 76.	6.7	41
47	Genome-Wide Association Study Identifies a New Locus at 7q21.13 Associated with Hepatitis B Virus-Related Hepatocellular Carcinoma. <i>Clinical Cancer Research</i> , 2018, 24, 906-915.	7.0	37
48	Genetic Variation of the Human $\alpha$ -2-Heremans-Schmid Glycoprotein (AHSG) Gene Associated with the Risk of SARS-CoV Infection. <i>PLoS ONE</i> , 2011, 6, e23730.	2.5	37
49	HECT ubiquitin ligase Smurf1 targets the tumor suppressor ING2 for ubiquitination and degradation. <i>FEBS Letters</i> , 2010, 584, 3005-3012.	2.8	34
50	Functional Polymorphism -31C/G in the Promoter of BIRC5 Gene and Risk of Nasopharyngeal Carcinoma among Chinese. <i>PLoS ONE</i> , 2011, 6, e16748.	2.5	32
51	A proteomic and phosphoproteomic landscape of KRAS mutant cancers identifies combination therapies. <i>Molecular Cell</i> , 2021, 81, 4076-4090.e8.	9.7	31
52	Linkage Disequilibrium and Haplotype Architecture for two ABC Transporter Genes (ABCC1 and ABCG2) in Chinese Population: Implications for Pharmacogenomic Association Studies. <i>Annals of Human Genetics</i> , 2004, 68, 563-573.	0.8	30
53	A functional tandem-repeats polymorphism in the downstream of TERT is associated with the risk of nasopharyngeal carcinoma in Chinese population. <i>BMC Medicine</i> , 2011, 9, 106.	5.5	29
54	The GTPase-activating protein GIT2 protects against colitis by negatively regulating Toll-like receptor signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8883-8888.	7.1	28

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55	Itch promotes the neddylation of JunB and regulates JunB-dependent transcription. Cellular Signalling, 2016, 28, 1186-1195.	3.6	25
56	TiO <sub>2</sub> with Tandem Fractionation (TAFT): An Approach for Rapid, Deep, Reproducible, and High-Throughput Phosphoproteome Analysis. Journal of Proteome Research, 2018, 17, 710-721.	3.7	25
57	ZNF498 promotes hepatocellular carcinogenesis by suppressing p53-mediated apoptosis and ferroptosis via the attenuation of p53 Ser46 phosphorylation. Journal of Experimental and Clinical Cancer Research, 2022, 41, 79.	8.6	25
58	Proteomics Links Ubiquitin Chain Topology Change to Transcription Factor Activation. Molecular Cell, 2019, 76, 126-137.e7.	9.7	24
59	CAPER: a Chromosome-Assembled human Proteome browser. Journal of Proteome Research, 2013, 12, 179-186.	3.7	22
60	SILVER: an efficient tool for stable isotope labeling LC-MS data quantitative analysis with quality control methods. Bioinformatics, 2014, 30, 586-587.	4.1	22
61	Molecular subtyping of cancer and nomination of kinase candidates for inhibition with phosphoproteomics: Reanalysis of CPTAC ovarian cancer. EBioMedicine, 2019, 40, 305-317.	6.1	21
62	Comprehensive assessment showed no associations of variants at the SLC10A1 locus with susceptibility to persistent HBV infection among Southern Chinese. Scientific Reports, 2017, 7, 46490.	3.3	20
63	Identification of noninvasive diagnostic biomarkers for hepatocellular carcinoma by urinary proteomics. Journal of Proteomics, 2020, 225, 103780.	2.4	20
64	Lack of support for an association between CLEC4M homozygosity and protection against SARS coronavirus infection. Nature Genetics, 2007, 39, 692-693.	21.4	19
65	Genomic gain of <i>RRS1</i> promotes hepatocellular carcinoma through reducing the RPL11-MDM2-p53 signaling. Science Advances, 2021, 7, .	10.3	19
66	A Non-Synonymous Single Nucleotide Polymorphism in the HJURP Gene Associated with Susceptibility to Hepatocellular Carcinoma among Chinese. PLoS ONE, 2016, 11, e0148618.	2.5	18
67	Common variations in TERT-CLPTM1L locus are reproducibly associated with the risk of nasopharyngeal carcinoma in Chinese populations. Oncotarget, 2016, 7, 759-770.	1.8	18
68	NEDL2 is an essential regulator of enteric neural development and GDNF/Ret signaling. Cellular Signalling, 2015, 27, 578-586.	3.6	16
69	Phosphoproteomics Enables Molecular Subtyping and Nomination of Kinase Candidates for Individual Patients of Diffuse-Type Gastric Cancer. IScience, 2019, 22, 44-57.	4.1	16
70	Argonaute 2 and nasopharyngeal carcinoma: a genetic association study and functional analysis. BMC Cancer, 2015, 15, 862.	2.6	15
71	Pulmonary expression of <i>CYP2A13</i> and <i>ABCB1</i> is regulated by FOXA2, and their genetic interaction is associated with lung cancer. FASEB Journal, 2015, 29, 1986-1998.	0.5	15
72	Proteome-wide Mapping of Endogenous SUMOylation Sites in Mouse Testis. Molecular and Cellular Proteomics, 2017, 16, 717-727.	3.8	15

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73	NEDL2 regulates enteric nervous system and kidney development in its Nedd8 ligase activity-dependent manner. <i>Oncotarget</i> , 2016, 7, 31440-31453.	1.8	15
74	Association between the functional polymorphism Ile31Phe in the <i>AURKA</i> gene and susceptibility of hepatocellular carcinoma in chronic hepatitis B virus carriers. <i>Oncotarget</i> , 2017, 8, 54904-54912.	1.8	14
75	Artificial MicroRNA-Mediated <i>Tgfr2</i> and <i>Pdgfrb</i> Co-Silencing Ameliorates Carbon Tetrachloride-Induced Hepatic Fibrosis in Mice. <i>Human Gene Therapy</i> , 2019, 30, 179-196.	2.7	13
76	ARF-dependent regulation of ATM and p53 associated KZNF (Apak) protein activity in response to oncogenic stress. <i>FEBS Letters</i> , 2010, 584, 3909-3915.	2.8	11
77	A Functional Polymorphism in <i>MIR196A2</i> Is Associated with Risk and Progression of Nasopharyngeal Carcinoma in the Chinese Population. <i>Genetic Testing and Molecular Biomarkers</i> , 2014, 18, 149-155.	0.7	11
78	Proteomic analysis reveals key differences between squamous cell carcinomas and adenocarcinomas across multiple tissues. <i>Nature Communications</i> , 2022, 13, .	12.8	11
79	Transcriptome and proteome of human hepatocellular carcinoma reveal shared metastatic pathways with significant genes. <i>Proteomics</i> , 2015, 15, 1793-1800.	2.2	10
80	Activation of mTORC1 by LSECtin in macrophages directs intestinal repair in inflammatory bowel disease. <i>Cell Death and Disease</i> , 2020, 11, 918.	6.3	10
81	Revealing the metabolic characteristics of human embryonic stem cells by genome-scale metabolic modeling. <i>FEBS Letters</i> , 2018, 592, 3670-3682.	2.8	9
82	KRAB-containing zinc finger protein ZNF496 inhibits breast cancer cell proliferation by selectively repressing ER $\alpha$ activity. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 841-853.	1.9	9
83	Transcription Factor Response Elements on Tip: A Sensitive Approach for Large-Scale Endogenous Transcription Factor Quantitative Identification. <i>Analytical Chemistry</i> , 2016, 88, 11990-11994.	6.5	8
84	Rapid development of proteomics in China: from the perspective of the Human Liver Proteome Project and technology development. <i>Science China Life Sciences</i> , 2014, 57, 1162-1171.	4.9	7
85	Mapping and analyzing the human liver proteome: progress and potential. <i>Expert Review of Proteomics</i> , 2016, 13, 833-843.	3.0	7
86	Association of <i>MCP1</i> promoter polymorphism with susceptibility to nasopharyngeal carcinoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 6661-6670.	2.6	7
87	Lifeomics leads the age of grand discoveries. <i>Science China Life Sciences</i> , 2013, 56, 201-212.	4.9	6
88	Ubiquitin Linkage Specificity of Deubiquitinases Determines Cyclophilin Nuclear Localization and Degradation. <i>IScience</i> , 2020, 23, 100984.	4.1	5
89	Deubiquitinase Ubp3 enhances the proteasomal degradation of key enzymes in sterol homeostasis. <i>Journal of Biological Chemistry</i> , 2021, 296, 100348.	3.4	5
90	Trans-acting non-synonymous variant of FOXA1 predisposes to hepatocellular carcinoma through modulating FOXA1-ER $\alpha$ transcriptional program and may have undergone natural selection. <i>Carcinogenesis</i> , 2020, 41, 146-158.	2.8	3

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91	Proteome-wide profiling of transcriptional machinery on accessible chromatin with biotinylated transposons. <i>Science Advances</i> , 2021, 7, eabh1022.	10.3	3
92	Comprehensive Profiling for Histone H4 of Human Liver Cells Using High Resolution LTQ-Orbitrap Mass Spectrometry. <i>Chinese Journal of Chemistry</i> , 2011, 29, 171-177.	4.9	2
93	Identification of KAP-1-associated complexes negatively regulating the Ey and $\beta^2$ -major globin genes in the $\beta^2$ -globin locus. <i>Journal of Proteomics</i> , 2013, 80, 132-144.	2.4	2
94	Exploration of Target Spaces in the Human Genome for Protein and Peptide Drugs. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 780-794.	6.9	2
95	Iterative Non-m/z-sharing Rule for Confident and Sensitive Protein Identification of Non-shotgun Proteomics. <i>Chinese Journal of Chemistry</i> , 2009, 27, 331-337.	4.9	0
96	Corrigendum to "E3 ubiquitin ligase Smurf1 targets the tumor suppressor ING2 for ubiquitination and degradation" [FEBS Lett. 584 (2010) 3005-3012]. <i>FEBS Letters</i> , 2011, 585, 266-266.	2.8	0
97	A Cytological Atlas of the Human Liver Proteome from PROTEOME <sup>SKY</sup> -LIVER <sup>Hu</sup> 2.0, a Publicly Available Database. <i>Journal of Proteome Research</i> , 0, , .	3.7	0