

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
all docs

98
docs citations

98
times ranked

14552
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	iProX in 2021: connecting proteomics data sharing with big data. <i>Nucleic Acids Research</i> , 2022, 50, D1522-D1527.	14.5	197
3	ZNF498 promotes hepatocellular carcinogenesis by suppressing p53-mediated apoptosis and ferroptosis via the attenuation of p53 Ser46 phosphorylation. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, 79.	8.6	25
4	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
5	Proteomic analysis reveals key differences between squamous cell carcinomas and adenocarcinomas across multiple tissues. <i>Nature Communications</i> , 2022, 13, .	12.8	11
6	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
7	Neddylation of PTEN regulates its nuclear import and promotes tumor development. <i>Cell Research</i> , 2021, 31, 291-311.	12.0	67
8	Deubiquitinase Ubp3 enhances the proteasomal degradation of key enzymes in sterol homeostasis. <i>Journal of Biological Chemistry</i> , 2021, 296, 100348.	3.4	5
9	Genomic gain of <i>RRS1</i> promotes hepatocellular carcinoma through reducing the RPL11-MDM2-p53 signaling. <i>Science Advances</i> , 2021, 7, .	10.3	19
10	Genome-wide association study of COVID-19 severity among the Chinese population. <i>Cell Discovery</i> , 2021, 7, 76.	6.7	41
11	A proteomic and phosphoproteomic landscape of KRAS mutant cancers identifies combination therapies. <i>Molecular Cell</i> , 2021, 81, 4076-4090.e8.	9.7	31
12	Proteome-wide profiling of transcriptional machinery on accessible chromatin with biotinylated transposons. <i>Science Advances</i> , 2021, 7, eabh1022.	10.3	3
13	Long Noncoding RNA p53-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
14	Trans-acting non-synonymous variant of FOXA1 predisposes to hepatocellular carcinoma through modulating FOXA1-ER1 transcriptional program and may have undergone natural selection. <i>Carcinogenesis</i> , 2020, 41, 146-158.	2.8	3
15	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301.	12.8	152
16	Ubiquitin Linkage Specificity of Deubiquitinases Determines Cyclophilin Nuclear Localization and Degradation. <i>Science</i> , 2020, 23, 100984.	4.1	5
17	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
18	Integrative Proteomic Characterization of Human Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 245-261.e17.	28.9	300

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19	Identification of noninvasive diagnostic biomarkers for hepatocellular carcinoma by urinary proteomics. <i>Journal of Proteomics</i> , 2020, 225, 103780.	2.4	20
20	Artificial MicroRNA-Mediated Tgfbr2 and Pdgfrb Co-Silencing Ameliorates Carbon Tetrachloride-Induced Hepatic Fibrosis in Mice. <i>Human Gene Therapy</i> , 2019, 30, 179-196.	2.7	13
21	Proteomics Links Ubiquitin Chain Topology Change to Transcription Factor Activation. <i>Molecular Cell</i> , 2019, 76, 126-137.e7.	9.7	24
22	Phosphoproteomics Enables Molecular Subtyping and Nomination of Kinase Candidates for Individual Patients of Diffuse-Type Gastric Cancer. <i>IScience</i> , 2019, 22, 44-57.	4.1	16
23	CKIP-1 limits foam cell formation and inhibits atherosclerosis by promoting degradation of Oct-1 by REG1 ³ . <i>Nature Communications</i> , 2019, 10, 425.	12.8	42
24	Neutrophils promote the development of reparative macrophages mediated by ROS to orchestrate liver repair. <i>Nature Communications</i> , 2019, 10, 1076.	12.8	231
25	Proteomics identifies new therapeutic targets of early-stage hepatocellular carcinoma. <i>Nature</i> , 2019, 567, 257-261.	27.8	613
26	Molecular subtyping of cancer and nomination of kinase candidates for inhibition with phosphoproteomics: Reanalysis of CPTAC ovarian cancer. <i>EBioMedicine</i> , 2019, 40, 305-317.	6.1	21
27	iProX: an integrated proteome resource. <i>Nucleic Acids Research</i> , 2019, 47, D1211-D1217.	14.5	1,001
28	Association of MCP1 promoter polymorphism with susceptibility to nasopharyngeal carcinoma. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 6661-6670.	2.6	7
29	A proteomic landscape of diffuse-type gastric cancer. <i>Nature Communications</i> , 2018, 9, 1012.	12.8	175
30	A proteomics landscape of circadian clock in mouse liver. <i>Nature Communications</i> , 2018, 9, 1553.	12.8	115
31	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
32	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
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	TiO ₂ with Tandem Fractionation (TAFT): An Approach for Rapid, Deep, Reproducible, and High-Throughput Phosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2018, 17, 710-721.	3.7	25
35	Dynamic ubiquitylation of Sox2 regulates proteostasis and governs neural progenitor cell differentiation. <i>Nature Communications</i> , 2018, 9, 4648.	12.8	47
36	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

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37	ER-associated ubiquitin ligase HRD1 programs liver metabolism by targeting multiple metabolic enzymes. <i>Nature Communications</i> , 2018, 9, 3659.	12.8	42
38	Mutually exclusive acetylation and ubiquitylation of the splicing factor SRSF5 control tumor growth. <i>Nature Communications</i> , 2018, 9, 2464.	12.8	77
39	KRAB-containing zinc finger protein ZNF496 inhibits breast cancer cell proliferation by selectively repressing ER α activity. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 841-853.	1.9	9
40	Comprehensive assessment showed no associations of variants at the SLC10A1 locus with susceptibility to persistent HBV infection among Southern Chinese. <i>Scientific Reports</i> , 2017, 7, 46490.	3.3	20
41	Proteome-wide Mapping of Endogenous SUMOylation Sites in Mouse Testis. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 717-727.	3.8	15
42	An integrated bioinformatics platform for investigating the human E3 ubiquitin ligase-substrate interaction network. <i>Nature Communications</i> , 2017, 8, 347.	12.8	151
43	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
44	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
45	Itch promotes the neddylation of JunB and regulates JunB-dependent transcription. <i>Cellular Signalling</i> , 2016, 28, 1186-1195.	3.6	25
46	Mapping and analyzing the human liver proteome: progress and potential. <i>Expert Review of Proteomics</i> , 2016, 13, 833-843.	3.0	7
47	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
48	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
49	A Cell-type-resolved Liver Proteome. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3190-3202.	3.8	83
50	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
51	A Non-Synonymous Single Nucleotide Polymorphism in the HJURP Gene Associated with Susceptibility to Hepatocellular Carcinoma among Chinese. <i>PLoS ONE</i> , 2016, 11, e0148618.	2.5	18
52	Common variations in TERT-CLPTM1L locus are reproducibly associated with the risk of nasopharyngeal carcinoma in Chinese populations. <i>Oncotarget</i> , 2016, 7, 759-770.	1.8	18
53	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
54	Argonaute 2 and nasopharyngeal carcinoma: a genetic association study and functional analysis. <i>BMC Cancer</i> , 2015, 15, 862.	2.6	15

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55	NEDL2 is an essential regulator of enteric neural development and GDNF/Ret signaling. <i>Cellular Signalling</i> , 2015, 27, 578-586.	3.6	16
56	Transcriptome and proteome of human hepatocellular carcinoma reveal shared metastatic pathways with significant genes. <i>Proteomics</i> , 2015, 15, 1793-1800.	2.2	10
57	Histone H3K9 demethylase JMJD1A modulates hepatic stellate cells activation and liver fibrosis by epigenetically regulating peroxisome proliferator-activated receptor β . <i>FASEB Journal</i> , 2015, 29, 1830-1841.	0.5	41
58	Pulmonary expression of <i>CYP2A13</i> and <i>ABCB1</i> is regulated by FOXA2, and their genetic interaction is associated with lung cancer. <i>FASEB Journal</i> , 2015, 29, 1986-1998.	0.5	15
59	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
60	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
61	Deubiquitylase OTUD3 regulates PTEN stability and suppresses tumorigenesis. <i>Nature Cell Biology</i> , 2015, 17, 1169-1181.	10.3	135
62	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
63	CKIP-1 regulates macrophage proliferation by inhibiting TRAF6-mediated Akt activation. <i>Cell Research</i> , 2014, 24, 742-761.	12.0	67
64	SILVER: an efficient tool for stable isotope labeling LC-MS data quantitative analysis with quality control methods. <i>Bioinformatics</i> , 2014, 30, 586-587.	4.1	22
65	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
66	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
67	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
68	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
69	Lifeomics leads the age of grand discoveries. <i>Science China Life Sciences</i> , 2013, 56, 201-212.	4.9	6
70	Identification of KAP-1-associated complexes negatively regulating the ϵ and β -major globin genes in the β -globin locus. <i>Journal of Proteomics</i> , 2013, 80, 132-144.	2.4	2
71	CAPER: a Chromosome-Assembled human Proteome browser. <i>Journal of Proteome Research</i> , 2013, 12, 179-186.	3.7	22
72	A Fast Workflow for Identification and Quantification of Proteomes. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2370-2380.	3.8	94

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73	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
74	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
75	Corrigendum to "HECT 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
76	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
77	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
78	Toward an understanding of the protein interaction network of the human liver. <i>Molecular Systems Biology</i> , 2011, 7, 536.	7.2	194
79	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
80	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
81	Genetic Variation of the Human α -2-Heremans-Schmid Glycoprotein (AHSG) Gene Associated with the Risk of SARS-CoV Infection. <i>PLoS ONE</i> , 2011, 6, e23730.	2.5	37
82	HECT ubiquitin ligase Smurf1 targets the tumor suppressor ING2 for ubiquitination and degradation. <i>FEBS Letters</i> , 2010, 584, 3005-3012.	2.8	34
83	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
84	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
85	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
86	Regulation of Cellular Metabolism by Protein Lysine Acetylation. <i>Science</i> , 2010, 327, 1000-1004.	12.6	1,642
87	A genome-wide association study of nasopharyngeal carcinoma identifies three new susceptibility loci. <i>Nature Genetics</i> , 2010, 42, 599-603.	21.4	374
88	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
89	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155
90	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

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91	Lack of support for an association between CLEC4M homozygosity and protection against SARS coronavirus infection. <i>Nature Genetics</i> , 2007, 39, 692-693.	21.4	19
92	Estrogen Receptor $\hat{\pm}$ Polymorphisms Associated With Susceptibility to Hepatocellular Carcinoma in Hepatitis B Virus Carriers. <i>Gastroenterology</i> , 2006, 130, 2001-2009.	1.3	74
93	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
94	Human Liver Proteome Project. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1841-1848.	3.8	67
95	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
96	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
97	A Cytological Atlas of the Human Liver Proteome from PROTEOME ^{SKY} -LIVER ^{Hu} 2.0, a Publicly Available Database. <i>Journal of Proteome Research</i> , 0, , .	3.7	0