

Ze-Xian Liu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2249758/publications.pdf>

Version: 2024-02-01

116
papers

12,342
citations

66343

42
h-index

27406

106
g-index

120
all docs

120
docs citations

120
times ranked

24235
citing authors

#	ARTICLE	IF	CITATIONS
1	qPTMplants: an integrative database of quantitative post-translational modifications in plants. <i>Nucleic Acids Research</i> , 2022, 50, D1491-D1499.	14.5	17
2	<i>Smad4</i> Deficiency Promotes Pancreatic Cancer Immunogenicity by Activating the Cancer-Associated DNA Sensing Signaling Axis. <i>Advanced Science</i> , 2022, 9, e2103029.	11.2	7
3	CircVPS13C promotes pituitary adenoma growth by decreasing the stability of IFITM1 mRNA via interacting with RRBP1. <i>Oncogene</i> , 2022, 41, 1550-1562.	5.9	12
4	Development and validation of a transcriptomics-based gene signature to predict distant metastasis and guide induction chemotherapy in locoregionally advanced nasopharyngeal carcinoma. <i>European Journal of Cancer</i> , 2022, 163, 26-34.	2.8	10
5	ADDAGMA: A database for domestic animal gut microbiome atlas. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 891-898.	4.1	10
6	Phosphorylated NFS1 weakens oxaliplatin-based chemosensitivity of colorectal cancer by preventing PANoptosis. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 54.	17.1	84
7	DrugCVar: a platform for evidence-based drug annotation for genetic variants in cancer. <i>Bioinformatics</i> , 2022, 38, 3094-3098.	4.1	1
8	Changing causes of death in persons with haematological cancers 1975-2016. <i>Leukemia</i> , 2022, 36, 1850-1860.	7.2	12
9	LncRNA TMPO-AS1 promotes esophageal squamous cell carcinoma progression by forming biomolecular condensates with FUS and p300 to regulate TMPO transcription. <i>Experimental and Molecular Medicine</i> , 2022, 54, 834-847.	7.7	14
10	gutMEGA: a database of the human gut MEtaGenome Atlas. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	22
11	CDK1/2/5 inhibition overcomes IFNG-mediated adaptive immune resistance in pancreatic cancer. <i>Gut</i> , 2021, 70, 890-899.	12.1	59
12	An Upstream Open Reading Frame in Phosphatase and Tensin Homolog Encodes a Circuit Breaker of Lactate Metabolism. <i>Cell Metabolism</i> , 2021, 33, 128-144.e9.	16.2	37
13	iCysMod: an integrative database for protein cysteine modifications in eukaryotes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	12
14	pCysMod: Prediction of Multiple Cysteine Modifications Based on Deep Learning Framework. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 617366.	3.7	21
15	Frequent amplification of HDAC genes and efficacy of HDAC inhibitor chidamide and PD-1 blockade combination in soft tissue sarcoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, e001696.		42
16	Dickkopf 1 impairs the tumor response to PD-1 blockade by inactivating CD8+ T cells in deficient mismatch repair colorectal cancer. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, e001498.		28
17	MYC-Activated LncRNA <i>MX1-AS1</i> Promotes the Progression of Colorectal Cancer by Stabilizing YB1. <i>Cancer Research</i> , 2021, 81, 2636-2650.	0.9	48
18	Fatal Infections Among Cancer Patients: A Population-Based Study in the United States. <i>Infectious Diseases and Therapy</i> , 2021, 10, 871-895.	4.0	38

#	ARTICLE	IF	CITATIONS
19	The lncRNA XIST/miRâ€125bâ€2â€3p axis modulates cell proliferation and chemotherapeutic sensitivity via targeting Wee1 in colorectal cancer. <i>Cancer Medicine</i> , 2021, 10, 2423-2441.	2.8	21
20	Loss of mitochondrial aconitase promotes colorectal cancer progression via SCD1-mediated lipid remodeling. <i>Molecular Metabolism</i> , 2021, 48, 101203.	6.5	22
21	DNA methylation regulator-mediated modification patterns and tumor microenvironment characterization in gastric cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 695-710.	5.1	25
22	FTO downregulation mediated by hypoxia facilitates colorectal cancer metastasis. <i>Oncogene</i> , 2021, 40, 5168-5181.	5.9	77
23	Insulin signaling regulates longevity through protein phosphorylation in <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2021, 12, 4568.	12.8	38
24	NSUN2-mediated RNA 5-methylcytosine promotes esophageal squamous cell carcinoma progression via LIN28B-dependent GRB2 mRNA stabilization. <i>Oncogene</i> , 2021, 40, 5814-5828.	5.9	59
25	Multiomics analysis of tumor mutational burden across cancer types. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5637-5646.	4.1	10
26	Inflammatory cytokineâ€regulated tRNA-derived fragment tRF-21 suppresses pancreatic ductal adenocarcinoma progression. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	36
27	iCAV: an integrative database of cancer-associated viruses. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	3.0	0
28	AMPKÎ±1 confers survival advantage of colorectal cancer cells under metabolic stress by promoting redox balance through the regulation of glutathione reductase phosphorylation. <i>Oncogene</i> , 2020, 39, 637-650.	5.9	16
29	CrossICC: iterative consensus clustering of cross-platform gene expression data without adjusting batch effect. <i>Briefings in Bioinformatics</i> , 2020, 21, 1818-1824.	6.5	8
30	Deep learning based prediction of reversible HAT/HDAC-specific lysine acetylation. <i>Briefings in Bioinformatics</i> , 2020, 21, 1798-1805.	6.5	24
31	Inhibition of fatty acid catabolism augments the efficacy of oxaliplatin-based chemotherapy in gastrointestinal cancers. <i>Cancer Letters</i> , 2020, 473, 74-89.	7.2	63
32	Circulating tumor DNA methylation profiles enable early diagnosis, prognosis prediction, and screening for colorectal cancer. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	260
33	Systematic analysis of the transcriptome in smallâ€cell carcinoma of the oesophagus reveals its immune microenvironment. <i>Clinical and Translational Immunology</i> , 2020, 9, e1173.	3.8	2
34	Direct Tumor Killing and Immunotherapy through Anti-SerpinB9 Therapy. <i>Cell</i> , 2020, 183, 1219-1233.e18.	28.9	54
35	Development and validation of metabolism-related gene signature in prognostic prediction of gastric cancer. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3217-3229.	4.1	14
36	VDRâ€SOX2 signaling promotes colorectal cancer stemness and malignancy in an acidic microenvironment. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 183.	17.1	30

#	ARTICLE	IF	CITATIONS
37	Ubiquitinome Profiling Reveals the Landscape of Ubiquitination Regulation in Rice Young Panicles. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 305-320.	6.9	18
38	METTL3 Promotes the Progression of Gastric Cancer via Targeting the MYC Pathway. <i>Frontiers in Oncology</i> , 2020, 10, 115.	2.8	76
39	Long noncoding RNA AGPG regulates PFKFB3-mediated tumor glycolytic reprogramming. <i>Nature Communications</i> , 2020, 11, 1507.	12.8	121
40	Inhibiting MARSs reduces hyperhomocysteinemia-associated neural tube and congenital heart defects. <i>EMBO Molecular Medicine</i> , 2020, 12, e9469.	6.9	21
41	Systematic Analysis of the Aberrances and Functional Implications of Ferroptosis in Cancer. <i>IScience</i> , 2020, 23, 101302.	4.1	128
42	ZIC2 is downregulated and represses tumor growth via the regulation of STAT3 in breast cancer. <i>International Journal of Cancer</i> , 2020, 147, 505-518.	5.1	20
43	Deep learning based prediction of species-specific protein S-glutathionylation sites. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140422.	2.3	17
44	Development and validation of the immune signature to predict distant metastasis in patients with nasopharyngeal carcinoma. , 2020, 8, e000205.		26
45	Evaluation of POLE and POLD1 Mutations as Biomarkers for Immunotherapy Outcomes Across Multiple Cancer Types. <i>JAMA Oncology</i> , 2019, 5, 1504.	7.1	287
46	The MRV11-AS1/ATF3 signaling loop sensitizes nasopharyngeal cancer cells to paclitaxel by regulating the Hippo-TAZ pathway. <i>Oncogene</i> , 2019, 38, 6065-6081.	5.9	47
47	Precise Prediction of Calpain Cleavage Sites and Their Aberrance Caused by Mutations in Cancer. <i>Frontiers in Genetics</i> , 2019, 10, 715.	2.3	26
48	Clonal Mutations Activate the NF- κ B Pathway to Promote Recurrence of Nasopharyngeal Carcinoma. <i>Cancer Research</i> , 2019, 79, 5930-5943.	0.9	32
49	Eukaryotic initiation factor 4A2 promotes experimental metastasis and oxaliplatin resistance in colorectal cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 196.	8.6	38
50	Excessive miR-25-3p maturation via N6-methyladenosine stimulated by cigarette smoke promotes pancreatic cancer progression. <i>Nature Communications</i> , 2019, 10, 1858.	12.8	242
51	Dysregulation, functional implications, and prognostic ability of the circadian clock across cancers. <i>Cancer Medicine</i> , 2019, 8, 1710-1720.	2.8	23
52	MSC-regulated lncRNA MACC1-AS1 promotes stemness and chemoresistance through fatty acid oxidation in gastric cancer. <i>Oncogene</i> , 2019, 38, 4637-4654.	5.9	201
53	IDDF2019-ABS-0316...Long non-coding RNA CRCAL-2 promotes gastric cancer metastasis by activating wnt/beta-catenin pathway via stabilizing the nuclear transport protein RAN. , 2019, , .		1
54	LncRNA LINRIS stabilizes IGF2BP2 and promotes the aerobic glycolysis in colorectal cancer. <i>Molecular Cancer</i> , 2019, 18, 174.	19.2	315

#	ARTICLE	IF	CITATIONS
55	PIWI-interacting RNA-36712 restrains breast cancer progression and chemoresistance by interaction with SEPW1 pseudogene SEPW1P RNA. <i>Molecular Cancer</i> , 2019, 18, 9.	19.2	139
56	qPhos: a database of protein phosphorylation dynamics in humans. <i>Nucleic Acids Research</i> , 2019, 47, D451-D458.	14.5	44
57	Modulation of Redox Homeostasis by Inhibition of MTHFD2 in Colorectal Cancer: Mechanisms and Therapeutic Implications. <i>Journal of the National Cancer Institute</i> , 2019, 111, 584-596.	6.3	125
58	Liquid biopsies to track trastuzumab resistance in metastatic HER2-positive gastric cancer. <i>Gut</i> , 2019, 68, 1152-1161.	12.1	118
59	The Heterogeneity Between Lynch-Associated and Sporadic MMR Deficiency in Colorectal Cancers. <i>Journal of the National Cancer Institute</i> , 2018, 110, 975-984.	6.3	32
60	ME1 Regulates NADPH Homeostasis to Promote Gastric Cancer Growth and Metastasis. <i>Cancer Research</i> , 2018, 78, 1972-1985.	0.9	86
61	The genomic landscape of small cell carcinoma of the esophagus. <i>Cell Research</i> , 2018, 28, 771-774.	12.0	23
62	THANATOS: an integrative data resource of proteins and post-translational modifications in the regulation of autophagy. <i>Autophagy</i> , 2018, 14, 296-310.	9.1	41
63	IDDF2018-ABS-0184â€¦LNCRNA AGPG regulates anabolism remodelling through affecting PFKFB3 stability in esc. , 2018, , .		0
64	The Clinical and Biomarker Association of Programmed Death Ligand 1 and its Spatial Heterogeneous Expression in Colorectal Cancer. <i>Journal of Cancer</i> , 2018, 9, 4325-4333.	2.5	16
65	PIWI-interacting RNA-54265 is oncogenic and a potential therapeutic target in colorectal adenocarcinoma. <i>Theranostics</i> , 2018, 8, 5213-5230.	10.0	115
66	Prediction of prkC-mediated protein serine/threonine phosphorylation sites for bacteria. <i>PLoS ONE</i> , 2018, 13, e0203840.	2.5	5
67	LncRNA CamK-A Regulates Ca ²⁺ -Signaling-Mediated Tumor Microenvironment Remodeling. <i>Molecular Cell</i> , 2018, 72, 71-83.e7.	9.7	119
68	Nicotinamide nucleotide transhydrogenase-mediated redox homeostasis promotes tumor growth and metastasis in gastric cancer. <i>Redox Biology</i> , 2018, 18, 246-255.	9.0	56
69	CPT1A-mediated fatty acid oxidation promotes colorectal cancer cell metastasis by inhibiting anoikis. <i>Oncogene</i> , 2018, 37, 6025-6040.	5.9	211
70	Quantitative Dynamics of Proteome, Acetylome, and Succinylome during Stem-Cell Differentiation into Hepatocyte-like Cells. <i>Journal of Proteome Research</i> , 2018, 17, 2491-2498.	3.7	7
71	GPS-PAIL: prediction of lysine acetyltransferase-specific modification sites from protein sequences. <i>Scientific Reports</i> , 2016, 6, 39787.	3.3	88
72	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1381-1396.	3.8	15

#	ARTICLE	IF	CITATIONS
73	Pyruvate Kinase M2 Activates mTORC1 by Phosphorylating AKT1S1. <i>Scientific Reports</i> , 2016, 6, 21524.	3.3	92
74	Computational screen and experimental validation of anti-influenza effects of quercetin and chlorogenic acid from traditional Chinese medicine. <i>Scientific Reports</i> , 2016, 6, 19095.	3.3	48
75	dbPAF: an integrative database of protein phosphorylation in animals and fungi. <i>Scientific Reports</i> , 2016, 6, 23534.	3.3	78
76	A new method for classifying different phenotypes of kidney transplantation. <i>Cell Biology and Toxicology</i> , 2016, 32, 323-332.	5.3	14
77	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	9.1	4,701
78	Enhanced Purification of Ubiquitinated Proteins by Engineered Tandem Hybrid Ubiquitin-binding Domains (ThUBDs). <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1381-1396.	3.8	44
79	dbPSP: a curated database for protein phosphorylation sites in prokaryotes. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav031.	3.0	23
80	Molecular Docking of Potential Inhibitors for Influenza H7N9. <i>Computational and Mathematical Methods in Medicine</i> , 2015, 2015, 1-8.	1.3	30
81	Phosphoproteomic Analysis of the Highly-Metastatic Hepatocellular Carcinoma Cell Line, MHCC97-H. <i>International Journal of Molecular Sciences</i> , 2015, 16, 4209-4225.	4.1	22
82	Reconfiguring phosphorylation signaling by genetic polymorphisms affects cancer susceptibility. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 187-202.	3.3	17
83	MiCroKiTS 4.0: a database of midbody, centrosome, kinetochore, telomere and spindle. <i>Nucleic Acids Research</i> , 2015, 43, D328-D334.	14.5	23
84	Analysis of phosphorylation sites on autophagy proteins. <i>Protein and Cell</i> , 2015, 6, 698-701.	11.0	5
85	Computational Identification of Protein Kinases and Kinase-Specific Substrates in Plants. <i>Methods in Molecular Biology</i> , 2015, 1306, 195-205.	0.9	1
86	Prediction of Serine/Threonine Phosphorylation Sites in Bacteria Proteins. <i>Advances in Experimental Medicine and Biology</i> , 2015, 827, 275-285.	1.6	10
87	dbPPT: a comprehensive database of protein phosphorylation in plants. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau121.	3.0	45
88	Systematic Analysis of the Phosphoproteome and Kinase-substrate Networks in the Mouse Testis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3626-3638.	3.8	38
89	GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. <i>Nucleic Acids Research</i> , 2014, 42, W325-W330.	14.5	417
90	HemI: A Toolkit for Illustrating Heatmaps. <i>PLoS ONE</i> , 2014, 9, e111988.	2.5	963

#	ARTICLE	IF	CITATIONS
91	Systematic characterization of small RNAome during zebrafish early developmental stages. BMC Genomics, 2014, 15, 117.	2.8	27
92	EKPD: a hierarchical database of eukaryotic protein kinases and protein phosphatases. Nucleic Acids Research, 2014, 42, D496-D502.	14.5	52
93	CPLM: a database of protein lysine modifications. Nucleic Acids Research, 2014, 42, D531-D536.	14.5	155
94	Computationally characterizing and comprehensive analysis of zinc-binding sites in proteins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 171-180.	2.3	10
95	Systematic analysis of the in situ crosstalk of tyrosine modifications reveals no additional natural selection on multiply modified residues. Scientific Reports, 2014, 4, 7331.	3.3	39
96	The human kinaseâ€‘substrate phosphorylation network rewired by genetic polymorphisms is heavily associated with cancers (984.3). FASEB Journal, 2014, 28, 984.3.	0.5	0
97	Towards a better understanding of the novel avian-origin H7N9 influenza A virus in China. Scientific Reports, 2013, 3, 2318.	3.3	17
98	Systematic analysis of the Plk-mediated phosphoregulation in eukaryotes. Briefings in Bioinformatics, 2013, 14, 344-360.	6.5	29
99	The structure of the ARE-binding domains of Hu antigen R (HuR) undergoes conformational changes during RNA binding. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 373-380.	2.5	90
100	UUCD: a family-based database of ubiquitin and ubiquitin-like conjugation. Nucleic Acids Research, 2013, 41, D445-D451.	14.5	99
101	Phosphoproteomicsâ€‘based network medicine. FEBS Journal, 2013, 280, 5696-5704.	4.7	16
102	Ubiquitin and Ubiquitin-Like Conjugations in Complex Diseases: A Computational Perspective. Translational Bioinformatics, 2013, , 171-187.	0.0	1
103	Systematic Analysis of Protein Phosphorylation Networks From Phosphoproteomic Data. Molecular and Cellular Proteomics, 2012, 11, 1070-1083.	3.8	161
104	GPS-MBA: Computational Analysis of MHC Class II Epitopes in Type 1 Diabetes. PLoS ONE, 2012, 7, e33884.	2.5	9
105	GPS-ARM: Computational Analysis of the APC/C Recognition Motif by Predicting D-Boxes and KEN-Boxes. PLoS ONE, 2012, 7, e34370.	2.5	44
106	GPS-PUP: computational prediction of pupylation sites in prokaryotic proteins. Molecular BioSystems, 2011, 7, 2737.	2.9	40
107	GPS-YNO2: computational prediction of tyrosine nitration sites in proteins. Molecular BioSystems, 2011, 7, 1197.	2.9	94
108	GPS-CCD: A Novel Computational Program for the Prediction of Calpain Cleavage Sites. PLoS ONE, 2011, 6, e19001.	2.5	94

#	ARTICLE	IF	CITATIONS
109	CPLA 1.0: an integrated database of protein lysine acetylation. <i>Nucleic Acids Research</i> , 2011, 39, D1029-D1034.	14.5	60
110	GPS 2.1: enhanced prediction of kinase-specific phosphorylation sites with an algorithm of motif length selection. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 255-260.	2.1	217
111	Computational Analysis of Phosphoproteomics: Progresses and Perspectives. <i>Current Protein and Peptide Science</i> , 2011, 12, 591-601.	1.4	13
112	GPS-SNO: Computational Prediction of Protein S-Nitrosylation Sites with a Modified GPS Algorithm. <i>PLoS ONE</i> , 2010, 5, e11290.	2.5	223
113	PhosSNP for Systematic Analysis of Genetic Polymorphisms That Influence Protein Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 623-634.	3.8	72
114	MiCroKit 3.0: an integrated database of midbody, centrosome and kinetochore. <i>Nucleic Acids Research</i> , 2010, 38, D155-D160.	14.5	27
115	A Summary of Computational Resources for Protein Phosphorylation. <i>Current Protein and Peptide Science</i> , 2010, 11, 485-496.	1.4	53
116	Computational Prediction of Post-Translational Modification Sites in Proteins. , 0, , .		13