

Chuan-Le Xiao

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

3,651
citations

257357

24
h-index

197736

49
g-index

62
all docs

62
docs citations

62
times ranked

6720
citing authors

#	ARTICLE	IF	CITATIONS
1	Immune cell profiling of COVID-19 patients in the recovery stage by single-cell sequencing. <i>Cell Discovery</i> , 2020, 6, 31.	3.1	644
2	N6-Methyladenine DNA Modification in the Human Genome. <i>Molecular Cell</i> , 2018, 71, 306-318.e7.	4.5	439
3	MECAT: fast mapping, error correction, and de novo assembly for single-molecule sequencing reads. <i>Nature Methods</i> , 2017, 14, 1072-1074.	9.0	357
4	Detection of DNA base modifications by deep recurrent neural network on Oxford Nanopore sequencing data. <i>Nature Communications</i> , 2019, 10, 2449.	5.8	237
5	A human circulating immune cell landscape in aging and COVID-19. <i>Protein and Cell</i> , 2020, 11, 740-770.	4.8	179
6	Efficient assembly of nanopore reads via highly accurate and intact error correction. <i>Nature Communications</i> , 2021, 12, 60.	5.8	166
7	Phosphoproteomic Analysis Reveals the Multiple Roles of Phosphorylation in Pathogenic Bacterium <i>Streptococcus pneumoniae</i> . <i>Journal of Proteome Research</i> , 2010, 9, 275-282.	1.8	164
8	DeepSignal: detecting DNA methylation state from Nanopore sequencing reads using deep-learning. <i>Bioinformatics</i> , 2019, 35, 4586-4595.	1.8	158
9	MethSMRT: an integrative database for DNA N6-methyladenine and N4-methylcytosine generated by single-molecular real-time sequencing. <i>Nucleic Acids Research</i> , 2017, 45, D85-D89.	6.5	111
10	Transfer RNAs Mediate the Rapid Adaptation of <i>Escherichia coli</i> to Oxidative Stress. <i>PLoS Genetics</i> , 2015, 11, e1005302.	1.5	93
11	CobB regulates <i>Escherichia coli</i> chemotaxis by deacetylating the response regulator CheY. <i>Molecular Microbiology</i> , 2010, 76, 1162-1174.	1.2	81
12	Global phosphoproteomic effects of natural tyrosine kinase inhibitor, genistein, on signaling pathways. <i>Proteomics</i> , 2010, 10, 976-986.	1.3	80
13	MDR: an integrative DNA N6-methyladenine and N4-methylcytosine modification database for Rosaceae. <i>Horticulture Research</i> , 2019, 6, 78.	2.9	77
14	Phosphoproteome analysis of the pathogenic bacterium <i>Helicobacter pylori</i> reveals overrepresentation of tyrosine phosphorylation and multiply phosphorylated proteins. <i>Proteomics</i> , 2011, 11, 1449-1461.	1.3	59
15	Genome-wide detection of cytosine methylations in plant from Nanopore data using deep learning. <i>Nature Communications</i> , 2021, 12, 5976.	5.8	47
16	Subcellular proteomics revealed the epithelial-mesenchymal transition phenotype in lung cancer. <i>Proteomics</i> , 2011, 11, 429-439.	1.3	44
17	Putative copper- and zinc-binding motifs in <i>Streptococcus pneumoniae</i> identified by immobilized metal affinity chromatography and mass spectrometry. <i>Proteomics</i> , 2011, 11, 3288-3298.	1.3	42
18	FANSe2: A Robust and Cost-Efficient Alignment Tool for Quantitative Next-Generation Sequencing Applications. <i>PLoS ONE</i> , 2014, 9, e94250.	1.1	42

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19	Transcriptomic and proteomic approach to studying SNX2112-induced K562 cells apoptosis and anti-leukemia activity in K562-NOD/SCID mice. <i>FEBS Letters</i> , 2009, 583, 1859-1866.	1.3	40
20	FANSe: an accurate algorithm for quantitative mapping of large scale sequencing reads. <i>Nucleic Acids Research</i> , 2012, 40, e83-e83.	6.5	39
21	Putative cobalt- and nickel-binding proteins and motifs in <i>Streptococcus pneumoniae</i> . <i>Metalomics</i> , 2013, 5, 928.	1.0	37
22	Quantitative Phosphoproteomics of Proteasome Inhibition in Multiple Myeloma Cells. <i>PLoS ONE</i> , 2010, 5, e13095.	1.1	28
23	Compacting a synthetic yeast chromosome arm. <i>Genome Biology</i> , 2021, 22, 5.	3.8	28
24	Phosphoproteomic analysis of primary human multiple myeloma cells. <i>Journal of Proteomics</i> , 2010, 73, 1381-1390.	1.2	25
25	Bacterial Proteome of <i>Streptococcus pneumoniae</i> Through Multidimensional Separations Coupled with LC-MS/MS. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 477-482.	1.0	22
26	Integrated single-cell analysis revealed immune dynamics during Ad5-nCoV immunization. <i>Cell Discovery</i> , 2021, 7, 64.	3.1	22
27	Comparative proteomic analysis to discover potential therapeutic targets in human multiple myeloma. <i>Proteomics - Clinical Applications</i> , 2009, 3, 1348-1360.	0.8	21
28	Phosphoproteomic Analysis of Protein Phosphorylation Networks in <i>Tetrahymena thermophila</i> , a Model Single-celled Organism. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 503-519.	2.5	21
29	N6-Methyladenine DNA modification in <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> genome. <i>Scientific Reports</i> , 2018, 8, 16272.	1.6	18
30	Proteomic Analysis of Membrane Proteins from <i>Streptococcus pneumoniae</i> with Multiple Separation Methods Plus High Accuracy Mass Spectrometry. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 683-694.	1.0	16
31	Characterization of Phosphoproteins in Gastric Cancer Secretome. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 83-90.	1.0	15
32	Identification of novel signaling components in genistein-regulated signaling pathways by quantitative phosphoproteomics. <i>Journal of Proteomics</i> , 2011, 75, 695-707.	1.2	15
33	Applications and potentials of nanopore sequencing in the (epi)genome and (epi)transcriptome era. <i>Innovation(China)</i> , 2021, 2, 100153.	5.2	15
34	Binomial Probability Distribution Model-Based Protein Identification Algorithm for Tandem Mass Spectrometry Utilizing Peak Intensity Information. <i>Journal of Proteome Research</i> , 2013, 12, 328-335.	1.8	14
35	N6-Methyladenine DNA Modification in the Woodland Strawberry (<i>Fragaria vesca</i>) Genome Reveals a Positive Relationship With Gene Transcription. <i>Frontiers in Genetics</i> , 2019, 10, 1288.	1.1	14
36	Phosphoproteome profile of human lung cancer cell line A549. <i>Molecular BioSystems</i> , 2011, 7, 472-479.	2.9	13

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37	DNA N6-Methyladenosine modification role in transmitted variations from genomic DNA to RNA in <i>Herrania umbratica</i> . <i>BMC Genomics</i> , 2019, 20, 508.	1.2	11
38	A new method for measuring functional similarity of microRNAs. <i>Journal of Integrated OMICS</i> , 2011, 1, .	0.5	8
39	Lipoprotein FtsB in <i>Streptococcus pyogenes</i> Binds Ferrichrome in Two Steps with Residues Tyr137 and Trp204 as Critical Ligands. <i>PLoS ONE</i> , 2013, 8, e65682.	1.1	8
40	Low-cost, Low-bias and Low-input RNA-seq with High Experimental Verifiability based on Semiconductor Sequencing. <i>Scientific Reports</i> , 2017, 7, 1053.	1.6	8
41	ISODb: A Comprehensive Database of Full-Length Isoforms Generated by Iso-Seq. <i>International Journal of Genomics</i> , 2018, 2018, 1-6.	0.8	8
42	Environmental Water and Sediment Microbial Communities Shape Intestine Microbiota for Host Health: The Central Dogma in an Anthropogenic Aquaculture Ecosystem. <i>Frontiers in Microbiology</i> , 2021, 12, 772149.	1.5	8
43	Identification of ubiquitinated proteins from human multiple myeloma U266 cells by proteomics. <i>Biomedical and Environmental Sciences</i> , 2011, 24, 422-30.	0.2	8
44	Dispec: A Novel Peptide Scoring Algorithm Based on Peptide Matching Discriminability. <i>PLoS ONE</i> , 2013, 8, e62724.	1.1	7
45	Detection of Abundant Proteins in Multiple Myeloma Cells by Proteomics. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 005-009.	0.4	6
46	Genomic Elucidation of a COVID-19 Resurgence and Local Transmission of SARS-CoV-2 in Guangzhou, China. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0007921.	1.8	5
47	Editorial: Biomedical Data Visualization: Methods and Applications. <i>Frontiers in Genetics</i> , 2022, 13, 890775.	1.1	2
48	SCSIt: A high-efficiency preprocessing tool for single-cell sequencing data from SPLiT-seq. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4574-4580.	1.9	1
49	A survey on <i>de novo</i> assembly methods for single-molecular sequencing. <i>Quantitative Biology</i> , 2020, 8, 203-215.	0.3	0
50	Genomic Elucidation of a COVID-19 Resurgence and Local Transmission of SARS-CoV-2 in Guangzhou, China. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0