

Li Chen

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,688
citations

430874

18
h-index

395702

33
g-index

41
all docs

41
docs citations

41
times ranked

3624
citing authors

#	ARTICLE	IF	CITATIONS
1	Accurate identification of circRNA landscape and complexity reveals their pivotal roles in human oligodendroglia differentiation. <i>Genome Biology</i> , 2022, 23, 48.	8.8	14
2	Exploiting deep transfer learning for the prediction of functional non-coding variants using genomic sequence. <i>Bioinformatics</i> , 2022, 38, 3164-3172.	4.1	9
3	A novel deep learning method for predictive modeling of microbiome data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	18
4	Genome-wide circadian rhythm detection methods: systematic evaluations and practical guidelines. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	24
5	National trends in prescription proton pump inhibitor use and expenditure in the United States in 2002-2017. <i>Journal of the American Pharmacists Association: JAPhA</i> , 2021, 61, 87-94.e7.	1.5	19
6	5-hydroxymethylcytosine is dynamically regulated during forebrain organoid development and aberrantly altered in Alzheimer's disease. <i>Cell Reports</i> , 2021, 35, 109042.	6.4	24
7	WEVar: a novel statistical learning framework for predicting noncoding regulatory variants. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	5
8	circMeta: a unified computational framework for genomic feature annotation and differential expression analysis of circular RNAs. <i>Bioinformatics</i> , 2020, 36, 539-545.	4.1	17
9	Ethnicity-specific and overlapping alterations of brain hydroxymethylome in Alzheimer's disease. <i>Human Molecular Genetics</i> , 2020, 29, 149-158.	2.9	11
10	Application of topic models to a compendium of ChIP-Seq datasets uncovers recurrent transcriptional regulatory modules. <i>Bioinformatics</i> , 2020, 36, 2352-2358.	4.1	2
11	In vitro and ex vivo gene expression profiling reveals differential kinetic response of HSPs and UPR genes is associated with PI resistance in multiple myeloma. <i>Blood Cancer Journal</i> , 2020, 10, 78.	6.2	9
12	powmic: an R package for power assessment in microbiome case-control studies. <i>Bioinformatics</i> , 2020, 36, 3563-3565.	4.1	7
13	Generic levothyroxine initiation and substitution among Medicare and Medicaid populations: a new user cohort study. <i>Endocrine</i> , 2020, 68, 336-348.	2.3	3
14	Destin: toolkit for single-cell analysis of chromatin accessibility. <i>Bioinformatics</i> , 2019, 35, 3818-3820.	4.1	26
15	A Bayesian mixture model for clustering droplet-based single-cell transcriptomic data from population studies. <i>Nature Communications</i> , 2019, 10, 1649.	12.8	56
16	Abstract LB-266: A novel computational combination-therapy prediction algorithm (secDrug) identifies the Namp1 inhibitor FK866 reverses PI-resistant multiple myeloma. , 2019, , .		0
17	Abstract 2947: Discovering novel secondary drug combinations in sex hormone-related cancers using large-scale pharmacogenomics databases through computational modeling and molecular genetics. , 2019, , .		0
18	Ten-Eleven Translocation Proteins Modulate the Response to Environmental Stress in Mice. <i>Cell Reports</i> , 2018, 25, 3194-3203.e4.	6.4	46

#	ARTICLE	IF	CITATIONS
19	A Phylogeny-Regularized Sparse Regression Model for Predictive Modeling of Microbial Community Data. <i>Frontiers in Microbiology</i> , 2018, 9, 3112.	3.5	20
20	Predictive Modeling of Microbiome Data Using a Phylogeny-Regularized Generalized Linear Mixed Model. <i>Frontiers in Microbiology</i> , 2018, 9, 1391.	3.5	35
21	GMPr: A robust normalization method for zero-inflated count data with application to microbiome sequencing data. <i>PeerJ</i> , 2018, 6, e4600.	2.0	168
22	Tet2 loss leads to hypermutagenicity in haematopoietic stem/progenitor cells. <i>Nature Communications</i> , 2017, 8, 15102.	12.8	88
23	DNA N6-methyladenine is dynamically regulated in the mouse brain following environmental stress. <i>Nature Communications</i> , 2017, 8, 1122.	12.8	182
24	Ten-eleven translocation 2 interacts with forkhead box O3 and regulates adult neurogenesis. <i>Nature Communications</i> , 2017, 8, 15903.	12.8	82
25	Using DIVAN to assess disease/trait-associated single nucleotide variants in genome-wide scale. <i>BMC Research Notes</i> , 2017, 10, 530.	1.4	10
26	Sex-specific hippocampal 5-hydroxymethylcytosine is disrupted in response to acute stress. <i>Neurobiology of Disease</i> , 2016, 96, 54-66.	4.4	24
27	Molecular signatures associated with ZIKV exposure in human cortical neural progenitors. <i>Nucleic Acids Research</i> , 2016, 44, 8610-8620.	14.5	155
28	DIVAN: accurate identification of non-coding disease-specific risk variants using multi-omics profiles. <i>Genome Biology</i> , 2016, 17, 252.	8.8	67
29	5-Hydroxymethylcytosine-mediated alteration of transposon activity associated with the exposure to adverse in utero environments in human. <i>Human Molecular Genetics</i> , 2016, 25, 2208-2219.	2.9	25
30	traseR: an R package for performing trait-associated SNP enrichment analysis in genomic intervals. <i>Bioinformatics</i> , 2016, 32, 1214-1216.	4.1	23
31	Genome-wide alterations in hippocampal 5-hydroxymethylcytosine links plasticity genes to acute stress. <i>Neurobiology of Disease</i> , 2016, 86, 99-108.	4.4	48
32	Combined use of spatial restraint stress and middle cerebral artery occlusion is a novel model of post-stroke depression in mice. <i>Scientific Reports</i> , 2015, 5, 16751.	3.3	32
33	Altering 5-hydroxymethylcytosine modification impacts ischemic brain injury. <i>Human Molecular Genetics</i> , 2015, 24, 5855-5866.	2.9	57
34	A novel statistical method for quantitative comparison of multiple ChIP-seq datasets. <i>Bioinformatics</i> , 2015, 31, 1889-1896.	4.1	48
35	Small Molecules Efficiently Reprogram Human Astroglial Cells into Functional Neurons. <i>Cell Stem Cell</i> , 2015, 17, 735-747.	11.1	250
36	Combined Loss of Tet1 and Tet2 Promotes B Cell, but Not Myeloid Malignancies, in Mice. <i>Cell Reports</i> , 2015, 13, 1692-1704.	6.4	83