

Zhenguo Lin

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,829
citations

430442

18
h-index

377514

34
g-index

44
all docs

44
docs citations

44
times ranked

2960
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct roles of nucleosome sliding and histone modifications in controlling the fidelity of transcription initiation. <i>RNA Biology</i> , 2021, 18, 1-11.	1.5	1
2	The origin and evolution of a distinct mechanism of transcription initiation in yeasts. <i>Genome Research</i> , 2021, 31, 51-63.	2.4	18
3	Transcriptome analysis provides genome annotation and expression profiles in the central nervous system of <i>Lymnaea stagnalis</i> at different ages. <i>BMC Genomics</i> , 2021, 22, 637.	1.2	5
4	TSSr: an R package for comprehensive analyses of TSS sequencing data. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab108.	1.5	6
5	Development-specific transcriptomic profiling suggests new mechanisms for anoxic survival in the ventricle of overwintering turtles. <i>Journal of Experimental Biology</i> , 2020, 223, .	0.8	9
6	Parallel Concerted Evolution of Ribosomal Protein Genes in Fungi and Its Adaptive Significance. <i>Molecular Biology and Evolution</i> , 2020, 37, 455-468.	3.5	14
7	Origins and Stepwise Expansion of R2R3-MYB Transcription Factors for the Terrestrial Adaptation of Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 575360.	1.7	11
8	Gap Junction Coding Innexin in <i>Lymnaea stagnalis</i> : Sequence Analysis and Characterization in Tissues and the Central Nervous System. <i>Frontiers in Synaptic Neuroscience</i> , 2020, 12, 1.	1.3	11
9	Origin and Evolution of the 2019 Novel Coronavirus. <i>Clinical Infectious Diseases</i> , 2020, 71, 882-883.	2.9	168
10	Genome sequences of horticultural plants: past, present, and future. <i>Horticulture Research</i> , 2019, 6, 112.	2.9	108
11	Quantifying the RNA cap epitranscriptome reveals novel caps in cellular and viral RNA. <i>Nucleic Acids Research</i> , 2019, 47, e130-e130.	6.5	124
12	YeastTSS: an integrative web database of yeast transcription start sites. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	34
13	Pervasive and dynamic transcription initiation in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 2019, 29, 1198-1210.	2.4	53
14	Mitochondrial Genome Variation Affects Multiple Respiration and Nonrespiration Phenotypes in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2019, 211, 773-786.	1.2	15
15	Ventricular transcriptomic changes induced by cold acclimation in the painted turtle suggests epigenetic-mediated transcriptional remodeling. <i>FASEB Journal</i> , 2019, 33, 726.4.	0.2	0
16	Heterogeneous rates of genome rearrangement contributed to the disparity of species richness in Ascomycota. <i>BMC Genomics</i> , 2018, 19, 282.	1.2	17
17	Identification of a novel fused gene family implicates convergent evolution in eukaryotic calcium signaling. <i>BMC Genomics</i> , 2018, 19, 306.	1.2	4
18	The Sequenced Angiosperm Genomes and Genome Databases. <i>Frontiers in Plant Science</i> , 2018, 9, 418.	1.7	110

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19	Effects of nitrogen metabolism on growth and aflatoxin biosynthesis in <i>Aspergillus flavus</i> . <i>Journal of Hazardous Materials</i> , 2017, 324, 691-700.	6.5	49
20	The WRKY Transcription Factor Family in Model Plants and Crops. <i>Critical Reviews in Plant Sciences</i> , 2017, 36, 311-335.	2.7	231
21	Origin and mechanism of crassulacean acid metabolism in orchids as implied by comparative transcriptomics and genomics of the carbon fixation pathway. <i>Plant Journal</i> , 2016, 86, 175-185.	2.8	45
22	Genomic Evolution of <i>Saccharomyces cerevisiae</i> under Chinese Rice Wine Fermentation. <i>Genome Biology and Evolution</i> , 2014, 6, 2516-2526.	1.1	28
23	Comparative Genomics and Evolutionary Genetics of Yeast Carbon Metabolism. , 2014, , 97-120.		0
24	Identifying Cis-Regulatory Changes Involved in the Evolution of Aerobic Fermentation in Yeasts. <i>Genome Biology and Evolution</i> , 2013, 5, 1065-1078.	1.1	14
25	Evolution After Whole-Genome Duplication: A Network Perspective. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2049-2057.	0.8	15
26	Evolution of 5' Untranslated Region Length and Gene Expression Reprogramming in Yeasts. <i>Molecular Biology and Evolution</i> , 2012, 29, 81-89.	3.5	48
27	Comparative analysis of somatic copy-number alterations across different human cancer types reveals two distinct classes of breakpoint hotspots. <i>Human Molecular Genetics</i> , 2012, 21, 4957-4965.	1.4	15
28	Expansion of Hexose Transporter Genes Was Associated with the Evolution of Aerobic Fermentation in Yeasts. <i>Molecular Biology and Evolution</i> , 2011, 28, 131-142.	3.5	82
29	The Evolution of Aerobic Fermentation in <i>Schizosaccharomyces pombe</i> Was Associated with Regulatory Reprogramming but not Nucleosome Reorganization. <i>Molecular Biology and Evolution</i> , 2011, 28, 1407-1413.	3.5	11
30	The spatial distribution of cis regulatory elements in yeast promoters and its implications for transcriptional regulation. <i>BMC Genomics</i> , 2010, 11, 581.	1.2	42
31	Phylogenetic detection of numerous gene duplications shared by animals, fungi and plants. <i>Genome Biology</i> , 2010, 11, R38.	13.9	20
32	Detecting positive selection in the budding yeast genome. <i>Journal of Evolutionary Biology</i> , 2009, 22, 2430-2437.	0.8	19
33	Ultraconserved coding regions outside the homeobox of mammalian Hox genes. <i>BMC Evolutionary Biology</i> , 2008, 8, 260.	3.2	17
34	The origins and early evolution of DNA mismatch repair genes—multiple horizontal gene transfers and co-evolution. <i>Nucleic Acids Research</i> , 2007, 35, 7591-7603.	6.5	94
35	Origins and evolution of the <i>recA/RAD51</i> gene family: Evidence for ancient gene duplication and endosymbiotic gene transfer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10328-10333.	3.3	268
36	The <i>AtRAD51C</i> Gene Is Required for Normal Meiotic Chromosome Synapsis and Double-Stranded Break Repair in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2005, 138, 965-976.	2.3	90