

Xuemei Lu

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,668
citations

471371

17
h-index

330025

37
g-index

52
all docs

52
docs citations

52
times ranked

3244
citing authors

#	ARTICLE	IF	CITATIONS
1	Extremely high genetic diversity in a single tumor points to prevalence of non-Darwinian cell evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6496-505.	3.3	313
2	Two Evolutionary Histories in the Genome of Rice: the Roles of Domestication Genes. <i>PLoS Genetics</i> , 2011, 7, e1002100.	1.5	188
3	Age-related immune clearance of hepatitis B virus infection requires the establishment of gut microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2175-2180.	3.3	175
4	Genomic incompatibilities in the diploid and tetraploid offspring of the goldfish \times common carp cross. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1327-1332.	3.3	119
5	The Ecology and Evolution of Cancer: The Ultra-Microevolutionary Process. <i>Annual Review of Genetics</i> , 2016, 50, 347-369.	3.2	86
6	The dynamics of DNA methylation fidelity during mouse embryonic stem cell self-renewal and differentiation. <i>Genome Research</i> , 2014, 24, 1296-1307.	2.4	72
7	From asymmetrical to balanced genomic diversification during rediploidization: Subgenomic evolution in allotetraploid fish. <i>Science Advances</i> , 2020, 6, eaaz7677.	4.7	59
8	Evolutionary transition between invertebrates and vertebrates via methylation reprogramming in embryogenesis. <i>National Science Review</i> , 2019, 6, 993-1003.	4.6	58
9	Functional Conservation of Both CDS- and 3'UTR-Located MicroRNA Binding Sites between Species. <i>Molecular Biology and Evolution</i> , 2015, 32, 623-628.	3.5	42
10	New Insights into the Evolutionary Rate of Hepatitis B Virus at Different Biological Scales. <i>Journal of Virology</i> , 2015, 89, 3512-3522.	1.5	33
11	<i>Mycobacterium tuberculosis</i> clinical isolates carry mutational signatures of host immune environments. <i>Science Advances</i> , 2020, 6, eaba4901.	4.7	33
12	Free-living human cells reconfigure their chromosomes in the evolution back to uni-cellularity. <i>ELife</i> , 2017, 6, .	2.8	31
13	Transcriptome sequencing reveals genetic mechanisms underlying the transition between the laying and brooding phases and gene expression changes associated with divergent reproductive phenotypes in chickens. <i>Molecular Biology Reports</i> , 2016, 43, 977-989.	1.0	29
14	Genome sequences reveal global dispersal routes and suggest convergent genetic adaptations in seahorse evolution. <i>Nature Communications</i> , 2021, 12, 1094.	5.8	29
15	On the founder effect in COVID-19 outbreaks: how many infected travelers may have started them all?. <i>National Science Review</i> , 2021, 8, nwaa246.	4.6	27
16	Evolutionary analysis and lineage designation of SARS-CoV-2 genomes. <i>Science Bulletin</i> , 2021, 66, 2297-2311.	4.3	26
17	Histone Demethylase KDM4B Promotes DNA Damage by Activating Long Interspersed Nuclear Element-1. <i>Cancer Research</i> , 2019, 79, 86-98.	0.4	25
18	Is the evolution in tumors Darwinian or non-Darwinian?. <i>National Science Review</i> , 2018, 5, 15-17.	4.6	24

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19	The twin-beginnings of COVID-19 in Asia and Europe—one prevails quickly. <i>National Science Review</i> , 2022, 9, nwab223.	4.6	22
20	Ultrasensitive and high-efficiency screen of de novo low-frequency mutations by o2n-seq. <i>Nature Communications</i> , 2017, 8, 15335.	5.8	20
21	On the origin of SARS-CoV-2—The blind watchmaker argument. <i>Science China Life Sciences</i> , 2021, 64, 1560-1563.	2.3	18
22	Deciphering the heterogeneity in DNA methylation patterns during stem cell differentiation and reprogramming. <i>BMC Genomics</i> , 2014, 15, 978.	1.2	17
23	Integrative single-cell omics analyses reveal epigenetic heterogeneity in mouse embryonic stem cells. <i>PLoS Computational Biology</i> , 2018, 14, e1006034.	1.5	17
24	The heterogeneity of plasma miRNA profiles in hepatocellular carcinoma patients and the exploration of diagnostic circulating miRNAs for hepatocellular carcinoma. <i>PLoS ONE</i> , 2019, 14, e0211581.	1.1	15
25	De novo assembly of highly polymorphic metagenomic data using in situ generated reference sequences and a novel BLAST-based assembly pipeline. <i>BMC Bioinformatics</i> , 2017, 18, 223.	1.2	14
26	Genetic Load and Potential Mutational Meltdown in Cancer Cell Populations. <i>Molecular Biology and Evolution</i> , 2019, 36, 541-552.	3.5	14
27	The Runaway Evolution of SARS-CoV-2 Leading to the Highly Evolved Delta Strain. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	14
28	Pseudo-Sanger sequencing: massively parallel production of long and near error-free reads using NGS technology. <i>BMC Genomics</i> , 2013, 14, 711.	1.2	12
29	Genome-wide analysis reveals molecular convergence underlying domestication in 7 bird and mammals. <i>BMC Genomics</i> , 2020, 21, 204.	1.2	12
30	The use of SARS-CoV-2-related coronaviruses from bats and pangolins to polarize mutations in SARS-Cov-2. <i>Science China Life Sciences</i> , 2020, 63, 1608-1611.	2.3	12
31	Ultra-precise detection of mutations by droplet-based amplification of circularized DNA. <i>BMC Genomics</i> , 2016, 17, 214.	1.2	11
32	Using ultra-sensitive next generation sequencing to dissect DNA damage-induced mutagenesis. <i>Scientific Reports</i> , 2016, 6, 25310.	1.6	10
33	Multi-omics Analysis of Primary Cell Culture Models Reveals Genetic and Epigenetic Basis of Intratumoral Phenotypic Diversity. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 576-589.	3.0	10
34	A Direct Test of Selection in Cell Populations Using the Diversity in Gene Expression within Tumors. <i>Molecular Biology and Evolution</i> , 2017, 34, 1730-1742.	3.5	9
35	Exome sequencing reveals the genetic landscape and frequent inactivation of <i>PCDHB3</i> in Chinese rectal cancers. <i>Journal of Pathology</i> , 2018, 245, 222-234.	2.1	9
36	Direct measurement of pervasive weak repression by microRNAs and their role at the network level. <i>BMC Genomics</i> , 2018, 19, 362.	1.2	9

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37	Variation in the life history strategy underlies functional diversity of tumors. National Science Review, 2021, 8, nwaa124.	4.6	7
38	TDP43 promotes stemness of breast cancer stem cells through CD44 variant splicing isoforms. Cell Death and Disease, 2022, 13, 428.	2.7	7
39	Epigenetic regulation of neuronal cell specification inferred with single cell "Omics" data. Computational and Structural Biotechnology Journal, 2020, 18, 942-952.	1.9	6
40	siRNAs with decreased off-target effect facilitate the identification of essential genes in cancer cells. Oncotarget, 2015, 6, 21603-21613.	0.8	6
41	Sex, sex chromosomes and gene expression. BMC Biology, 2011, 9, 30.	1.7	5
42	Birth and death of Mx genes and the presence/absence of genes regulating Mx transcription are correlated with the diversity of anti-pathogenicity in vertebrate species. Molecular Genetics and Genomics, 2019, 294, 121-133.	1.0	5
43	Evolution under Spatially Heterogeneous Selection in Solid Tumors. Molecular Biology and Evolution, 2022, 39, .	3.5	5
44	Virtual methylome dissection facilitated by single-cell analyses. Epigenetics and Chromatin, 2019, 12, 66.	1.8	4
45	Deep sequencing reveals the genomic characteristics of lung adenocarcinoma presenting as ground-glass nodules (GGNs). Translational Lung Cancer Research, 2021, 10, 1239-1255.	1.3	4
46	The concordance between the evolutionary trend and the clinical manifestation of the two SARS-CoV-2 variants. National Science Review, 2021, 8, nwab073.	4.6	2
47	Small Segmental Duplications in <i>Drosophila</i> "High Rate of Emergence and Elimination. Genome Biology and Evolution, 2019, 11, 486-496.	1.1	1
48	Genomic sequencing identifies a few mutations driving the independent origin of primary liver tumors in a chronic hepatitis murine model. PLoS ONE, 2017, 12, e0187551.	1.1	1