

# Xuan Li

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1079506/publications.pdf>

Version: 2024-02-01

42  
papers

3,061  
citations

361413  
20  
h-index

276875  
41  
g-index

42  
all docs

42  
docs citations

42  
times ranked

5675  
citing authors

#	ARTICLE	IF	CITATIONS
1	Expanding the Coverage of Metabolic Landscape in Cultivated Rice with Integrated Computational Approaches. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 702-714.	6.9	3
2	Vorinostat Corrects Cognitive and Non-Cognitive Symptoms in a Mouse Model of Fragile X Syndrome. <i>International Journal of Neuropsychopharmacology</i> , 2022, 25, 147-159.	2.1	3
3	Molecular dynamic simulation analysis of SARS-CoV-2 spike mutations and evaluation of ACE2 from pets and wild animals for infection risk. <i>Computational Biology and Chemistry</i> , 2022, 96, 107613.	2.3	7
4	DENA: training an authentic neural network model using Nanopore sequencing data of Arabidopsis transcripts for detection and quantification of N6-methyladenosine on RNA. <i>Genome Biology</i> , 2022, 23, 25.	8.8	30
5	Targeted inhibition of Zika virus infection in human cells by CRISPR-Cas13b. <i>Virus Research</i> , 2022, 312, 198707.	2.2	10
6	Revealing the novel complexity of plant long non-coding RNA by strand-specific and whole transcriptome sequencing for evolutionarily representative plant species. <i>BMC Genomics</i> , 2022, 23, 381.	2.8	3
7	Creating RNA Specific C-to-U Editase from APOBEC3A by Separation of Its Activities on DNA and RNA Substrates. <i>ACS Synthetic Biology</i> , 2021, 10, 1106-1115.	3.8	14
8	Revealing the Viral Community in the Hadal Sediment of the New Britain Trench. <i>Genes</i> , 2021, 12, 990.	2.4	2
9	Revealing the full biosphere structure and versatile metabolic functions in the deepest ocean sediment of the Challenger Deep. <i>Genome Biology</i> , 2021, 22, 207.	8.8	27
10	Rapid screening and identification of viral pathogens in metagenomic data. <i>BMC Medical Genomics</i> , 2021, 14, 289.	1.5	2
11	UV-B photoreceptor UVR8 interacts with MYB73/MYB77 to regulate auxin responses and lateral root development. <i>EMBO Journal</i> , 2020, 39, e101928.	7.8	97
12	Integrated metabolomics and transcriptomics study of traditional herb <i>Astragalus membranaceus</i> Bge. var. <i>mongolicus</i> (Bge.) Hsiao reveals global metabolic profile and novel phytochemical ingredients. <i>BMC Genomics</i> , 2020, 21, 697.	2.8	11
13	Transcriptome signature analysis repurposes trifluoperazine for the treatment of fragile X syndrome in mouse model. <i>Communications Biology</i> , 2020, 3, 127.	4.4	15
14	Is SARS-CoV-2 originated from laboratory? A rebuttal to the claim of formation via laboratory recombination. <i>Emerging Microbes and Infections</i> , 2020, 9, 545-547.	6.5	23
15	Evolution of the novel coronavirus from the ongoing Wuhan outbreak and modeling of its spike protein for risk of human transmission. <i>Science China Life Sciences</i> , 2020, 63, 457-460.	4.9	1,650
16	Interfering with retrotransposition by two types of CRISPR effectors: Cas12a and Cas13a. <i>Cell Discovery</i> , 2020, 6, 30.	6.7	6
17	Molecular simulation of SARS-CoV-2 spike protein binding to pangolin ACE2 or human ACE2 natural variants reveals altered susceptibility to infection. <i>Journal of General Virology</i> , 2020, 101, 921-924.	2.9	42
18	Accurate prediction of potential druggable proteins based on genetic algorithm and Bagging-SVM ensemble classifier. <i>Artificial Intelligence in Medicine</i> , 2019, 98, 35-47.	6.5	72

#	ARTICLE	IF	CITATIONS
19	Comparative transcriptomic analysis of the flower induction and development of the Lei bamboo ( <i>Phyllostachys violascens</i> ). <i>BMC Bioinformatics</i> , 2019, 20, 687.	2.6	14
20	Draft genome of the cotton aphid <i>Aphis gossypii</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2019, 105, 25-32.	2.7	55
21	Predicting drug-target interactions using Lasso with random forest based on evolutionary information and chemical structure. <i>Genomics</i> , 2019, 111, 1839-1852.	2.9	145
22	The Pentatricopeptide Repeat Protein SOT5/EMB2279 Is Required for Plastid <i>rpl2</i> and <i>trnK</i> Intron Splicing. <i>Plant Physiology</i> , 2018, 177, 684-697.	4.8	41
23	Transcriptomic and metabolic flux analyses reveal shift of metabolic patterns during rice grain development. <i>BMC Systems Biology</i> , 2018, 12, 47.	3.0	10
24	The LsrB Protein Is Required for <i>Agrobacterium tumefaciens</i> Interaction with Host Plants. <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 951-961.	2.6	12
25	A comprehensive study on cellular RNA editing activity in response to infections with different subtypes of influenza A viruses. <i>BMC Genomics</i> , 2018, 19, 925.	2.8	15
26	A survey on cellular RNA editing activity in response to <i>Candida albicans</i> infections. <i>BMC Genomics</i> , 2018, 19, 43.	2.8	4
27	Implementation of the CRISPR-Cas13a system in fission yeast and its repurposing for precise RNA editing. <i>Nucleic Acids Research</i> , 2018, 46, e90-e90.	14.5	52
28	Modelling BioNano optical data and simulation study of genome map assembly. <i>Bioinformatics</i> , 2018, 34, 3966-3974.	4.1	20
29	Global transcriptome analysis reveals extensive gene remodeling, alternative splicing and differential transcription profiles in non-seed vascular plant <i>Selaginella moellendorffii</i> . <i>BMC Genomics</i> , 2017, 18, 1042.	2.8	34
30	BioNano Genome Map Resource for <i>Oryza sativa</i> ssp. <i>japonica</i> and <i>indica</i> and Its Application in Rice Genome Sequence Correction and Gap Filling. <i>Molecular Plant</i> , 2017, 10, 895-898.	8.3	11
31	Global transcriptome analysis of <i>Huperzia serrata</i> and identification of critical genes involved in the biosynthesis of huperzine A. <i>BMC Genomics</i> , 2017, 18, 245.	2.8	31
32	Decipher the ancestry of the plant-specific LBD gene family. <i>BMC Genomics</i> , 2017, 18, 951.	2.8	27
33	The gene expression profiles in response to 102 traditional Chinese medicine (TCM) components: a general template for research on TCMs. <i>Scientific Reports</i> , 2017, 7, 352.	3.3	102
34	Molecular characterization and expression analysis of CS $\pm$ <sup>12</sup> defensin genes from the scorpion <i>Mesobuthus martensii</i> . <i>Bioscience Reports</i> , 2017, 37, .	2.4	6
35	Regulation of cysteine residues in LsrB proteins from <i>Sinorhizobium meliloti</i> under free-living and symbiotic oxidative stress. <i>Environmental Microbiology</i> , 2017, 19, 5130-5145.	3.8	20
36	The Landscape of A-to-I RNA Editome Is Shaped by Both Positive and Purifying Selection. <i>PLoS Genetics</i> , 2016, 12, e1006191.	3.5	72

#	ARTICLE	IF	CITATIONS
37	Development of INDEL Markers for Genetic Mapping Based on Whole Genome Resequencing in Soybean. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2793-2799.	1.8	45
38	Global Analysis Reveals the Crucial Roles of DNA Methylation during Rice Seed Development. <i>Plant Physiology</i> , 2015, 168, 1417-1432.	4.8	112
39	Genome-wide analysis of homeobox genes from <i>Mesobuthus martensii</i> reveals Hox gene duplication in scorpions. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 61, 25-33.	2.7	25
40	Global transcriptome and gene regulation network for secondary metabolite biosynthesis of tea plant ( <i>Camellia sinensis</i> ). <i>BMC Genomics</i> , 2015, 16, 560.	2.8	174
41	The evolutionary landscape of intergenic trans-splicing events in insects. <i>Nature Communications</i> , 2015, 6, 8734.	12.8	17
42	Expression Sensitivity Analysis of Human Disease Related Genes. <i>BioMed Research International</i> , 2013, 2013, 1-8.	1.9	0