

# Cristiane P Calixto

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7150472/publications.pdf>

Version: 2024-02-01

19  
papers

1,350  
citations

777949

13  
h-index

939365

18  
g-index

23  
all docs

23  
docs citations

23  
times ranked

2036  
citing authors

#	ARTICLE	IF	CITATIONS
1	3D RNA-seq: a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data for biologists. <i>RNA Biology</i> , 2021, 18, 1574-1587.	1.5	58
2	Reading between the Lines: RNA-seq Data Mining Reveals the Alternative Message of the Rice Leaf Transcriptome in Response to Heat Stress. <i>Plants</i> , 2021, 10, 1647.	1.6	12
3	Do ensino remoto emergencial ao ensino híbrido no curso de Ciências Biológicas: a nossa visão a partir do Instituto de Biociências da Universidade de São Paulo (IB-USP). <i>Medicina</i> , 2021, 54, .	0.0	0
4	Cold-Dependent Expression and Alternative Splicing of Arabidopsis Long Non-coding RNAs. <i>Frontiers in Plant Science</i> , 2019, 10, 235.	1.7	70
5	Alternative Splicing of Circadian Clock Genes Correlates With Temperature in Field-Grown Sugarcane. <i>Frontiers in Plant Science</i> , 2019, 10, 1614.	1.7	20
6	High-Resolution RT-PCR Analysis of Alternative Barley Transcripts. <i>Methods in Molecular Biology</i> , 2019, 1900, 269-281.	0.4	11
7	How does temperature affect splicing events? Isoform switching of splicing factors regulates splicing of <i>LATE ELONGATED HYPOCOTYL</i> ( <i>LHY</i> ). <i>Plant, Cell and Environment</i> , 2018, 41, 1539-1550.	2.8	25
8	Rapid and Dynamic Alternative Splicing Impacts the Arabidopsis Cold Response Transcriptome. <i>Plant Cell</i> , 2018, 30, 1424-1444.	3.1	294
9	A high quality Arabidopsis transcriptome for accurate transcript-level analysis of alternative splicing. <i>Nucleic Acids Research</i> , 2017, 45, 5061-5073.	6.5	262
10	TSIS: an R package to infer alternative splicing isoform switches for time-series data. <i>Bioinformatics</i> , 2017, 33, 3308-3310.	1.8	58
11	Evaluation and improvement of the regulatory inference for large co-expression networks with limited sample size. <i>BMC Systems Biology</i> , 2017, 11, 62.	3.0	14
12	High-quality reference transcript datasets hold the key to transcript-specific RNA-seq analysis in plants. <i>New Phytologist</i> , 2017, 213, 525-530.	3.5	35
13	Alternative Splicing of Barley Clock Genes in Response to Low Temperature. <i>PLoS ONE</i> , 2016, 11, e0168028.	1.1	39
14	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. <i>Nature Genetics</i> , 2016, 48, 1024-1030.	9.4	259
15	Monitoring Alternative Splicing Changes in Arabidopsis Circadian Clock Genes. <i>Methods in Molecular Biology</i> , 2016, 1398, 119-132.	0.4	11
16	At RTD – a comprehensive reference transcript dataset resource for accurate quantification of transcript-specific expression in Arabidopsis thaliana. <i>New Phytologist</i> , 2015, 208, 96-101.	3.5	50
17	Evolutionary Relationships Among Barley and Arabidopsis Core Circadian Clock and Clock-Associated Genes. <i>Journal of Molecular Evolution</i> , 2015, 80, 108-119.	0.8	59
18	Plant U13 orthologues and orphan snoRNAs identified by RNomics of RNA from Arabidopsis nucleoli. <i>Nucleic Acids Research</i> , 2010, 38, 3054-3067.	6.5	39

#	ARTICLE	IF	CITATIONS
19	Analyses of Sexual Reproductive Success in Transgenic and/or Mutant Plants. Journal of Integrative Plant Biology, 2009, 51, 719-726.	4.1	2