

# Keithanne Mockaitis

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/537779/publications.pdf>

Version: 2024-02-01

18  
papers

1,503  
citations

567281

15  
h-index

839539

18  
g-index

19  
all docs

19  
docs citations

19  
times ranked

2365  
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel Ca <sup>2+</sup> -binding protein that can rapidly transduce auxin responses during root growth. <i>PLoS Biology</i> , 2019, 17, e3000085.	5.6	35
2	Stilbenoid prenyltransferases define key steps in the diversification of peanut phytoalexins. <i>Journal of Biological Chemistry</i> , 2018, 293, 28-46.	3.4	36
3	Population genomic analyses of the chocolate tree, <i>Theobroma cacao</i> L., provide insights into its domestication process. <i>Communications Biology</i> , 2018, 1, 167.	4.4	73
4	A Specialized Diacylglycerol Acyltransferase Contributes to the Extreme Medium-Chain Fatty Acid Content of <i>Cuphea</i> Seed Oil. <i>Plant Physiology</i> , 2017, 174, 97-109.	4.8	44
5	A Stilbenoid-Specific Prenyltransferase Utilizes Dimethylallyl Pyrophosphate from the Plastidic Terpenoid Pathway. <i>Plant Physiology</i> , 2016, 171, 2483-2498.	4.8	18
6	The Zinc-Finger Protein SOP1 Is Required for a Subset of the Nuclear Exosome Functions in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2016, 12, e1005817.	3.5	36
7	Structurally divergent lysophosphatidic acid acyltransferases with high selectivity for saturated medium chain fatty acids from <i>Cuphea</i> seeds. <i>Plant Journal</i> , 2015, 84, 1021-1033.	5.7	32
8	A Long-Read Transcriptome Assembly of Cotton ( <i>Gossypium hirsutum</i> L.) and Intraspecific Single Nucleotide Polymorphism Discovery. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0068.	2.8	12
9	Deep sequencing of the Mexican avocado transcriptome, an ancient angiosperm with a high content of fatty acids. <i>BMC Genomics</i> , 2015, 16, 599.	2.8	69
10	Toward production of jet fuel functionality in oilseeds: identification of FatB acyl-acyl carrier protein thioesterases and evaluation of combinatorial expression strategies in <i>Camelina</i> seeds. <i>Journal of Experimental Botany</i> , 2015, 66, 4251-4265.	4.8	80
11	Making a chocolate chip: development and evaluation of a 6K SNP array for <i>Theobroma cacao</i> . <i>DNA Research</i> , 2015, 22, 279-291.	3.4	46
12	FEATnotator: A tool for integrated annotation of sequence features and variation, facilitating interpretation in genomics experiments. <i>Methods</i> , 2015, 79-80, 11-17.	3.8	7
13	Oil biosynthesis in a basal angiosperm: transcriptome analysis of <i>Persea Americana</i> mesocarp. <i>BMC Plant Biology</i> , 2015, 15, 203.	3.6	96
14	Development and Evaluation of Quality Metrics for Bioinformatics Analysis of Viral Insertion Site Data Generated Using High Throughput Sequencing. <i>Biomedicines</i> , 2014, 2, 195-210.	3.2	1
15	<i>Camelina</i> seed transcriptome: a tool for meal and oil improvement and translational research. <i>Plant Biotechnology Journal</i> , 2013, 11, 759-769.	8.3	166
16	Auxin Receptors and Plant Development: A New Signaling Paradigm. <i>Annual Review of Cell and Developmental Biology</i> , 2008, 24, 55-80.	9.4	547
17	Integrating transcriptional controls for plant cell expansion. <i>Genome Biology</i> , 2004, 5, 245.	9.6	20
18	Auxin induces mitogenic activated protein kinase (MAPK) activation in roots of <i>Arabidopsis</i> seedlings. <i>Plant Journal</i> , 2000, 24, 785-796.	5.7	185