

Michael A Seidel

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8174251/publications.pdf>

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14
papers

1,268
citations

623734

14
h-index

1058476

14
g-index

15
all docs

15
docs citations

15
times ranked

2462
citing authors

#	ARTICLE	IF	CITATIONS
1	European maize genomes highlight intraspecies variation in repeat and gene content. <i>Nature Genetics</i> , 2020, 52, 950-957.	21.4	84
2	Tracing the ancestry of modern bread wheats. <i>Nature Genetics</i> , 2019, 51, 905-911.	21.4	230
3	The <i>de Novo</i> Reference Genome and Transcriptome Assemblies of the Wild Tomato Species <i>Solanum chilense</i> Highlights Birth and Death of NLR Genes Between Tomato Species. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3933-3941.	1.8	37
4	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. <i>Genome Biology</i> , 2016, 17, 137.	8.8	51
5	PGSB PlantsDB: updates to the database framework for comparative plant genome research. <i>Nucleic Acids Research</i> , 2016, 44, D1141-D1147.	14.5	79
6	A Genome-Wide Survey of Date Palm Cultivars Supports Two Major Subpopulations in <i>Phoenix dactylifera</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1429-1438.	1.8	58
7	Parallel Selection Revealed by Population Sequencing in Chicken. <i>Genome Biology and Evolution</i> , 2015, 7, 3299-3306.	2.5	25
8	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. <i>BMC Genomics</i> , 2014, 15, 823.	2.8	242
9	RNASeqExpressionBrowser—a web interface to browse and visualize high-throughput expression data. <i>Bioinformatics</i> , 2014, 30, 2519-2520.	4.1	23
10	BSTA: a targeted approach combines bulked segregant analysis with next-generation sequencing and de novo transcriptome assembly for SNP discovery in sunflower. <i>BMC Genomics</i> , 2013, 14, 628.	2.8	43
11	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. <i>Frontiers in Plant Science</i> , 2012, 3, 5.	3.6	73
12	From RNA-seq to large-scale genotyping - genomics resources for rye (<i>Secale cereale</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 131.	3.6	109
13	De novo 454 sequencing of barcoded BAC pools for comprehensive gene survey and genome analysis in the complex genome of barley. <i>BMC Genomics</i> , 2009, 10, 547.	2.8	69
14	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. <i>Genome Biology</i> , 2009, 10, R94.	9.6	130