

Karine Alix

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,847
citations

361413

20
h-index

580821

25
g-index

28
all docs

28
docs citations

28
times ranked

2240
citing authors

#	ARTICLE	IF	CITATIONS
1	Editorial: Mobile Elements and Plant Genome Evolution, Comparative Analyzes and Computational Tools. <i>Frontiers in Plant Science</i> , 2021, 12, 735134.	3.6	12
2	Yam genomics supports West Africa as a major cradle of crop domestication. <i>Science Advances</i> , 2019, 5, eaaw1947.	10.3	71
3	Assessing the Response of Small RNA Populations to Allopolyploidy Using Resynthesized <i>Brassica napus</i> Allotetraploids. <i>Molecular Biology and Evolution</i> , 2019, 36, 709-726.	8.9	22
4	Systematic comparison of small RNA library preparation protocols for next-generation sequencing. <i>BMC Genomics</i> , 2018, 19, 118.	2.8	93
5	Polyploidy and interspecific hybridization: partners for adaptation, speciation and evolution in plants. <i>Annals of Botany</i> , 2017, 120, 183-194.	2.9	306
6	Molecular basis of African yam domestication: analyses of selection point to root development, starch biosynthesis, and photosynthesis related genes. <i>BMC Genomics</i> , 2017, 18, 782.	2.8	20
7	Polyploidy and genome evolution. <i>Annals of Botany</i> , 2014, 113, vii-viii.	2.9	1
8	The bright side of transposons in crop evolution. <i>Briefings in Functional Genomics</i> , 2014, 13, 276-295.	2.7	106
9	Detection of Transposable Element Insertion Site Polymorphisms by Sequence-Specific Amplification Polymorphism (SSAP). <i>Bio-protocol</i> , 2014, 4, .	0.4	0
10	Allopolyploidy has a moderate impact on restructuring at three contrasting transposable element insertion sites in resynthesized <i>Brassica napus</i> allotetraploids. <i>New Phytologist</i> , 2013, 198, 593-604.	7.3	72
11	The evolution of flower development: current understanding and future challenges. <i>Annals of Botany</i> , 2011, 107, 1427-1431.	2.9	19
12	BraSto, a Stowaway MITE from <i>Brassica</i> : recently active copies preferentially accumulate in the gene space. <i>Plant Molecular Biology</i> , 2011, 77, 59-75.	3.9	50
13	Impact of transposable elements on the organization and function of allopolyploid genomes. <i>New Phytologist</i> , 2010, 186, 37-45.	7.3	233
14	Analysis of gene expression in resynthesized <i>Brassica napus</i> allotetraploids: transcriptional changes do not explain differential protein regulation. <i>New Phytologist</i> , 2010, 186, 216-227.	7.3	65
15	Principles and practices of plant genomics. Volume 2: Molecular breeding. <i>Annals of Botany</i> , 2009, 104, viii-viii.	2.9	0
16	Contrasting evolutionary patterns and target specificities among three Tourist-like MITE families in the maize genome. <i>Plant Molecular Biology</i> , 2009, 71, 99-114.	3.9	27
17	Repetitive sequence-derived markers tag centromeres and telomeres and provide insights into chromosome evolution in <i>Brassica napus</i> . <i>Chromosome Research</i> , 2008, 16, 683-700.	2.2	19
18	The CACTA transposon <i>Bot1</i> played a major role in <i>Brassica</i> genome divergence and gene proliferation. <i>Plant Journal</i> , 2008, 56, 1030-1044.	5.7	75

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19	Exploiting natural genetic diversity and mutant resources of <i>Arabidopsis thaliana</i> to study the <i>A. thaliana</i> / <i>Plasmodiophora brassicae</i> interaction. <i>Plant Breeding</i> , 2007, 126, 218-221.	1.9	47
20	Differential regulation of gene products in newly synthesized <i>Brassica napus</i> allotetraploids is not related to protein function nor subcellular localization. <i>BMC Genomics</i> , 2007, 8, 56.	2.8	36
21	The Genomic Organization of Retrotransposons in <i>Brassica oleracea</i> . <i>Plant Molecular Biology</i> , 2005, 59, 839-851.	3.9	40
22	The diversity of retroelements in diploid and allotetraploid <i>Brassica</i> species. <i>Plant Molecular Biology</i> , 2004, 54, 895-909.	3.9	42
23	From Diploids to Allopolyploids: The Emergence of Efficient Pairing Control Genes in Plants. <i>Critical Reviews in Plant Sciences</i> , 2004, 23, 21-45.	5.7	96
24	Inter-Alu-like species-specific sequences in the <i>Saccharum</i> complex. <i>Theoretical and Applied Genetics</i> , 1999, 99, 962-968.	3.6	41
25	Determination of basic chromosome numbers in the genus <i>Saccharum</i> by physical mapping of ribosomal RNA genes. <i>Genome</i> , 1998, 41, 221-225.	2.0	262
26	Isolation and characterization of a satellite DNA family in the <i>Saccharum</i> complex. <i>Genome</i> , 1998, 41, 854-864.	2.0	57
27	Isolation and characterization of a satellite DNA family in the <i>Saccharum</i> complex. <i>Genome</i> , 1998, 41, 854-864.	2.0	34