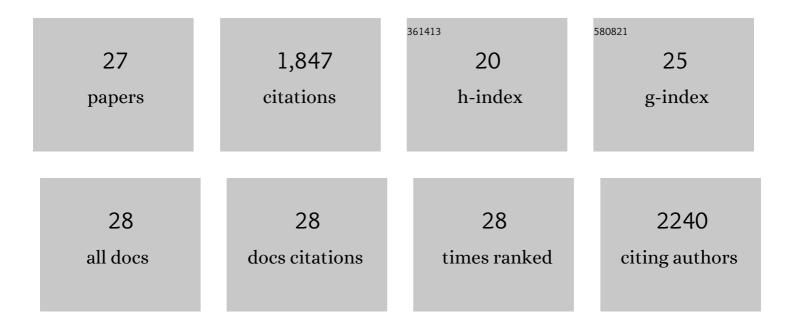
## Karine Alix

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6287466/publications.pdf Version: 2024-02-01



KADINE ALIY

#	Article	IF	CITATIONS
1	Editorial: Mobile Elements and Plant Genome Evolution, Comparative Analyzes and Computational Tools. Frontiers in Plant Science, 2021, 12, 735134.	3.6	12
2	Yam genomics supports West Africa as a major cradle of crop domestication. Science Advances, 2019, 5, eaaw1947.	10.3	71
3	Assessing the Response of Small RNA Populations to Allopolyploidy Using Resynthesized Brassica napus Allotetraploids. Molecular Biology and Evolution, 2019, 36, 709-726.	8.9	22
4	Systematic comparison of small RNA library preparation protocols for next-generation sequencing. BMC Genomics, 2018, 19, 118.	2.8	93
5	Polyploidy and interspecific hybridization: partners for adaptation, speciation and evolution in plants. Annals of Botany, 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. BMC Genomics, 2017, 18, 782.	2.8	20
7	Polyploidy and genome evolution. Annals of Botany, 2014, 113, vii-viii.	2.9	1
8	The bright side of transposons in crop evolution. Briefings in Functional Genomics, 2014, 13, 276-295.	2.7	106
9	Detection of Transposable Element Insertion Site Polymorphisms by Sequence-Specific Amplification Polymorphism (SSAP). Bio-protocol, 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. New Phytologist, 2013, 198, 593-604.	7.3	72
11	The evolution of flower development: current understanding and future challenges. Annals of Botany, 2011, 107, 1427-1431.	2.9	19
12	BraSto, a Stowaway MITE from Brassica: recently active copies preferentially accumulate in the gene space. Plant Molecular Biology, 2011, 77, 59-75.	3.9	50
13	Impact of transposable elements on the organization and function of allopolyploid genomes. New Phytologist, 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. New Phytologist, 2010, 186, 216-227.	7.3	65
15	Principles and practices of plant genomics. Volume 2: Molecular breeding. Annals of Botany, 2009, 104, viii-viii.	2.9	0
16	Contrasting evolutionary patterns and target specificities among three Tourist-like MITE families in the maize genome. Plant Molecular Biology, 2009, 71, 99-114.	3.9	27
17	Repetitive sequence-derived markers tag centromeres and telomeres and provide insights into chromosome evolution in Brassica napus. Chromosome Research, 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. Plant Journal, 2008, 56, 1030-1044.	5.7	75

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