

Andrea Zuccolo

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

13,116
citations

147726

31
h-index

197736

49
g-index

56
all docs

56
docs citations

56
times ranked

16522
citing authors

#	ARTICLE	IF	CITATIONS
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
2	Human gut microbiota in obesity and after gastric bypass. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2365-2370.	3.3	1,641
3	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
4	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	13.7	1,303
5	The high-quality draft genome of peach (<i>Prunus persica</i>) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013, 45, 487-494.	9.4	1,031
6	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 2014, 32, 656-662.	9.4	572
7	Gene duplication and exon shuffling by helitron-like transposons generate intraspecies diversity in maize. <i>Nature Genetics</i> , 2005, 37, 997-1002.	9.4	452
8	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
9	The genome sequence of African rice (<i>Oryza glaberrima</i>) and evidence for independent domestication. <i>Nature Genetics</i> , 2014, 46, 982-988.	9.4	342
10	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	6.5	295
11	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021, 184, 1156-1170.e14.	13.5	259
12	The Chinese pine genome and methylome unveil key features of conifer evolution. <i>Cell</i> , 2022, 185, 204-217.e14.	13.5	151
13	Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021, 14, 1757-1767.	3.9	133
14	Dynamic Evolution of <i>Oryza</i> Genomes Is Revealed by Comparative Genomic Analysis of a Genus-Wide Vertical Data Set. <i>Plant Cell</i> , 2009, 20, 3191-3209.	3.1	128
15	Transposable element distribution, abundance and role in genome size variation in the genus <i>Oryza</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 152.	3.2	115
16	Evolutionary dynamics of an ancient retrotransposon family provides insights into evolution of genome size in the genus <i>Oryza</i> . <i>Plant Journal</i> , 2007, 52, 342-351.	2.8	99
17	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	1.2	86
18	A platinum standard pan-genome resource that represents the population structure of Asian rice. <i>Scientific Data</i> , 2020, 7, 113.	2.4	86

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19	Functional and evolutionary genomic inferences in <i>Populus</i> through genome and population sequencing of American and European aspen. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10970-E10978.	3.3	84
20	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (<i>Phaseolus vulgaris</i> L.) Genome. Tropical Plant Biology, 2008, 1, 40-48.	1.0	70
21	The Amborella genome: an evolutionary reference for plant biology. Genome Biology, 2008, 9, 402.	13.9	67
22	RetrOryza: a database of the rice LTR-retrotransposons. Nucleic Acids Research, 2007, 35, D66-D70.	6.5	53
23	DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses. Nature Communications, 2016, 7, 12790.	5.8	51
24	A draft physical map of a D-genome cotton species (<i>Gossypium raimondii</i>). BMC Genomics, 2010, 11, 395.	1.2	48
25	Extreme Hypoxic Conditions Induce Selective Molecular Responses and Metabolic Reset in Detached Apple Fruit. Frontiers in Plant Science, 2016, 7, 146.	1.7	48
26	Analysis of transposons and repeat composition of the sunflower (<i>Helianthus annuus</i> L.) genome. Theoretical and Applied Genetics, 2010, 120, 491-508.	1.8	47
27	Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus <i>Oryza</i> . Plant Journal, 2010, 63, 990-1003.	2.8	47
28	Evolution of gene structure in the conifer <i>Picea glauca</i> : a comparative analysis of the impact of intron size. BMC Plant Biology, 2014, 14, 95.	1.6	46
29	LTR Retrotransposons Show Low Levels of Unequal Recombination and High Rates of Intraelement Gene Conversion in Large Plant Genomes. Genome Biology and Evolution, 2017, 9, 3449-3462.	1.1	45
30	Epigenetic patterns within the haplotype phased fig (<i>Ficus carica</i> L.) genome. Plant Journal, 2020, 102, 600-614.	2.8	43
31	Structured Motifs Search. Journal of Computational Biology, 2005, 12, 1065-1082.	0.8	34
32	Targeting environmental adaptation in the monocot model <i>Brachypodium distachyon</i> : a multi-faceted approach. BMC Genomics, 2014, 15, 801.	1.2	33
33	Comparative in silico analysis of EST-SSRs in angiosperm and gymnosperm tree genera. BMC Plant Biology, 2014, 14, 220.	1.6	29
34	A physical map for the <i>Amborella trichopoda</i> genome sheds light on the evolution of angiosperm genome structure. Genome Biology, 2011, 12, R48.	13.9	28
35	Construction of a nurse shark (<i>Ginglymostoma cirratum</i>) bacterial artificial chromosome (BAC) library and a preliminary genome survey. BMC Genomics, 2006, 7, 106.	1.2	27
36	The Ty1-copia LTR retroelement family PARTC is highly conserved in conifers over 200MY of evolution. Gene, 2015, 568, 89-99.	1.0	24

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37	A draft genome of sweet cherry (<i>Prunus avium</i> L.) reveals genome-wide and local effects of domestication. <i>Plant Journal</i> , 2020, 103, 1420-1432.	2.8	23
38	Re-sequencing of a virulent strain of <i>Campylobacter jejuni</i> NCTC11168 reveals potential virulence factors. <i>Research in Microbiology</i> , 2013, 164, 6-11.	1.0	16
39	Identification and characterization of abundant repetitive sequences in <i>Eragrostis tef</i> cv. Enatite genome. <i>BMC Plant Biology</i> , 2016, 16, 39.	1.6	16
40	Potential of Platinum Standard Reference Genomes to Exploit Natural Variation in the Wild Relatives of Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 579980.	1.7	15
41	Complete Genome Sequence of <i>Campylobacter jejuni</i> Strain S3. <i>Journal of Bacteriology</i> , 2011, 193, 1491-1492.	1.0	14
42	Characterization and chromosomal organization of satellite DNA sequences in <i>Picea abies</i> . <i>Genome</i> , 2008, 51, 705-713.	0.9	10
43	The <i>Oryza</i> Map Alignment Project (OMAP): A New Resource for Comparative Genome Studies within <i>Oryza</i> . , 2007, , 395-409.		9
44	Characterization of the chromosome complement of <i>Helianthus annuus</i> by in situ hybridization of a tandemly repeated DNA sequence. <i>Genome</i> , 2007, 50, 429-434.	0.9	9
45	Structured motifs search. , 2004, , .		7
46	Rapid and Differential Proliferation of the Ty3-Gypsy LTR Retrotransposon Atlantys in the Genus <i>Oryza</i> . <i>Rice</i> , 2008, 1, 85-99.	1.7	7
47	DNA Transposon Expansion is Associated with Genome Size Increase in Mudminnows. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	7
48	Assessing the Extent of Substitution Rate Variation of Retrotransposon Long Terminal Repeat Sequences in <i>Oryza sativa</i> and <i>Oryza glaberrima</i> . <i>Rice</i> , 2010, 3, 242-250.	1.7	5
49	Phylogenetic relationships between annual and perennial species of <i>Helianthus</i> : evolution of a tandem repeated DNA sequence and cytological hybridization experiments. <i>Genome</i> , 2008, 51, 1047-1053.	0.9	4
50	Genomic skimming for identification of medium/highly abundant transposable elements in <i>Arundo donax</i> and <i>Arundo plinii</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 157-171.	1.0	4
51	Repetitive Sequences. <i>Compendium of Plant Genomes</i> , 2016, , 115-123.	0.3	0
52	Transposable Elements in Spruce. <i>Compendium of Plant Genomes</i> , 2020, , 37-49.	0.3	0