

Tony Heitkam

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7261524/publications.pdf>

Version: 2024-02-01

28
papers

526
citations

687363

13
h-index

713466

21
g-index

34
all docs

34
docs citations

34
times ranked

573
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide analysis of long terminal repeat retrotransposons from the cranberry <i>Vaccinium macrocarpon</i> . <i>Journal of Berry Research</i> , 2022, 12, 165-185.	1.4	2
2	ECCsplorer: a pipeline to detect extrachromosomal circular DNA (eccDNA) from next-generation sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, 40.	2.6	36
3	Complete pan-plastome sequences enable high resolution phylogenetic classification of sugar beet and closely related crop wild relatives. <i>BMC Genomics</i> , 2022, 23, 113.	2.8	10
4	Ancient Artworks and Crocus Genetics Both Support Saffron's Origin in Early Greece. <i>Frontiers in Plant Science</i> , 2022, 13, 834416.	3.6	6
5	<i>Larix</i> species range dynamics in Siberia since the Last Glacial captured from sedimentary ancient DNA. <i>Communications Biology</i> , 2022, 5, .	4.4	10
6	The Cassandra retrotransposon landscape in sugar beet (<i>Beta vulgaris</i>) and related Amaranthaceae: recombination and re-shuffling lead to a high structural variability. <i>Annals of Botany</i> , 2021, 127, 91-109.	2.9	13
7	Can we have it all? Repurposing target capture for repeat genomics. A commentary on: "Aiming off the target: recycling target capture sequencing reads for investigating repetitive DNA". <i>Annals of Botany</i> , 2021, 128, iii-v.	2.9	0
8	TE Hub: A community-oriented space for sharing and connecting tools, data, resources, and methods for transposable element annotation. <i>Mobile DNA</i> , 2021, 12, 16.	3.6	13
9	Broken, silent, and in hiding: tamed endogenous pararetroviruses escape elimination from the genome of sugar beet (<i>Beta vulgaris</i>). <i>Annals of Botany</i> , 2021, 128, 281-299.	2.9	17
10	Comparative Repeat Profiling of Two Closely Related Conifers (<i>Larix decidua</i> and <i>Larix kaempferi</i>) Reveals High Genome Similarity With Only Few Fast-Evolving Satellite DNAs. <i>Frontiers in Genetics</i> , 2021, 12, 683668.	2.3	7
11	The conserved 3' ends of Angiosperm domain defines a superfamily of short interspersed nuclear elements (SINEs) in higher plants. <i>Plant Journal</i> , 2020, 101, 681-699.	5.7	8
12	Bioinformatic and Molecular Analysis of Satellite Repeat Diversity in <i>Vaccinium</i> Genomes. <i>Genes</i> , 2020, 11, 527.	2.4	10
13	Divergence of 3' ends as a driver of short interspersed nuclear element (SINE) evolution in the Salicaceae. <i>Plant Journal</i> , 2020, 103, 443-458.	5.7	6
14	Satellite DNA landscapes after allotetraploidization of quinoa (<i>Chenopodium quinoa</i>) reveal unique A and B subgenomes. <i>Plant Journal</i> , 2020, 103, 32-52.	5.7	29
15	Adding color to a century-old enigma: multi-color chromosome identification unravels the autotriploid nature of saffron (<i>Crocus sativus</i>) as a hybrid of wild <i>Crocus cartwrightianus</i> cytotypes. <i>New Phytologist</i> , 2019, 222, 1965-1980.	7.3	47
16	Balancing Retrospection and Visions: The Cytogenetics Group of the Society of Plant Breeding (GPZ) Came Together in Dresden. <i>Cytogenetic and Genome Research</i> , 2019, 159, 163-168.	1.1	0
17	FlexiDot: highly customizable, ambiguity-aware dotplots for visual sequence analyses. <i>Bioinformatics</i> , 2018, 34, 3575-3577.	4.1	60
18	Next-generation sequencing reveals differentially amplified tandem repeats as a major genome component of Northern Europe's oldest <i>Camellia japonica</i> . <i>Chromosome Research</i> , 2015, 23, 791-806.	2.2	24

#	ARTICLE	IF	CITATIONS
19	The diversification and activity of hAT transposons in Musa genomes. Chromosome Research, 2014, 22, 559-571.	2.2	14
20	TE-Tracker: systematic identification of transposition events through whole-genome resequencing. BMC Bioinformatics, 2014, 15, 377.	2.6	27
21	Profiling of extensively diversified plant <i>LINE</i> s reveals distinct plant-specific subclades. Plant Journal, 2014, 79, 385-397.	5.7	35
22	Highly diverse chromoviruses of Beta vulgaris are classified by chromodomains and chromosomal integration. Mobile DNA, 2013, 4, 8.	3.6	36
23	Evolutionary reshuffling in the Errantivirus lineage Elbe within the <i>Beta vulgaris</i> genome. Plant Journal, 2012, 72, 636-651.	5.7	26
24	The Ty1-copia families SALIRE and Cotzilla populating the Beta vulgaris genome show remarkable differences in abundance, chromosomal distribution, and age. Chromosome Research, 2010, 18, 247-263.	2.2	37
25	BNR – a LINE family from <i>Beta vulgaris</i> – contains a RRM domain in open reading frame 1 and defines a L1 sub-clade present in diverse plant genomes. Plant Journal, 2009, 59, 872-882.	5.7	23
26	A comparative analysis of two conserved motifs in bacterial poly(A) polymerase and CCA-adding enzyme. Nucleic Acids Research, 2008, 36, 5212-5220.	14.5	25
27	Application of retrotransposon-based Inter-SINE Amplified Polymorphism (ISAP) markers for the differentiation of common poplar genotypes. Canadian Journal of Forest Research, 0, , .	1.7	2
28	The function of two conserved elements in the bacterial Poly(A)Polymerase and CCA-adding enzyme. , 0, 2008, .		0