

Wirulda Pootakham

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

3,980
citations

331670

21
h-index

175258

52
g-index

54
all docs

54
docs citations

54
times ranked

5245
citing authors

#	ARTICLE	IF	CITATIONS
1	A chromosome-scale reference genome assembly of yellow mangrove (<i>Bruguiera parviflora</i>) reveals a whole genome duplication event associated with the Rhizophoraceae lineage. <i>Molecular Ecology Resources</i> , 2022, 22, 1939-1953.	4.8	13
2	A <i>de novo</i> reference assembly of the yellow mangrove <i>Ceriops zippeliana</i> genome. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	7
3	De Novo Reference Assembly of the Upriver Orange Mangrove (<i>Bruguiera sexangula</i>) Genome. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	8
4	Comparative Analysis and Phylogenetic Relationships of <i>Ceriops</i> Species (Rhizophoraceae) and <i>Avicennia lanata</i> (Acanthaceae): Insight into the Chloroplast Genome Evolution between Middle and Seaward Zones of Mangrove Forests. <i>Biology</i> , 2022, 11, 383.	2.8	10
5	The First Genetic Linkage Map of Winged Bean [<i>Psophocarpus tetragonolobus</i> (L.) DC.] and QTL Mapping for Flower-, Pod-, and Seed-Related Traits. <i>Plants</i> , 2022, 11, 500.	3.5	5
6	A SNP variation in an expansin (<i>EgExp4</i>) gene affects height in oil palm. <i>PeerJ</i> , 2022, 10, e13046.	2.0	4
7	Assembly of a hybrid mangrove, <i>Bruguiera hainesii</i> , and its two ancestral contributors, <i>Bruguiera cylindrica</i> and <i>Bruguiera gymnorhiza</i> . <i>Genomics</i> , 2022, 114, 110382.	2.9	5
8	Chromosome-level genome assembly of Indian mangrove (<i>Ceriops tagal</i>) revealed a genome-wide duplication event predating the divergence of Rhizophoraceae mangrove species. <i>Plant Genome</i> , 2022, 15, .	2.8	8
9	A chromosome-scale assembly of the black gram (<i>Vigna mungo</i>) genome. <i>Molecular Ecology Resources</i> , 2021, 21, 238-250.	4.8	33
10	De novo assemblies of <i>Luffa acutangula</i> and <i>Luffa cylindrica</i> genomes reveal an expansion associated with substantial accumulation of transposable elements. <i>Molecular Ecology Resources</i> , 2021, 21, 212-225.	4.8	23
11	A chromosome-level assembly of the black tiger shrimp (<i>Penaeus monodon</i>) genome facilitates the identification of growth-associated genes. <i>Molecular Ecology Resources</i> , 2021, 21, 1620-1640.	4.8	43
12	De novo chromosome-level assembly of the <i>Centella asiatica</i> genome. <i>Genomics</i> , 2021, 113, 2221-2228.	2.9	14
13	Taxonomic profiling of Symbiodiniaceae and bacterial communities associated with Indo-Pacific corals in the Gulf of Thailand using PacBio sequencing of full-length ITS and 16S rRNA genes. <i>Genomics</i> , 2021, 113, 2717-2729.	2.9	14
14	Identification of Candidate Gene-Based Markers for Girth Growth in Rubber Trees. <i>Plants</i> , 2021, 10, 1440.	3.5	3
15	Comparative Analysis of PacBio and Oxford Nanopore Sequencing Technologies for Transcriptomic Landscape Identification of <i>Penaeus monodon</i> . <i>Life</i> , 2021, 11, 862.	2.4	7
16	Complete chloroplast genome sequences of five <i>Bruguiera</i> species (Rhizophoraceae): comparative analysis and phylogenetic relationships. <i>PeerJ</i> , 2021, 9, e12268.	2.0	13
17	De novo Assembly of the Brain Coral <i>Platygyra sinensis</i> Genome. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	2
18	Transcriptome sequencing revealed the influence of blue light on the expression levels of light-stress response genes in <i>Centella asiatica</i> . <i>PLoS ONE</i> , 2021, 16, e0260468.	2.5	6

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19	The Genome and Transcriptome Analysis of the <i>Vigna mungo</i> Chloroplast. <i>Plants</i> , 2020, 9, 1247.	3.5	6
20	Assembly of the durian chloroplast genome using long PacBio reads. <i>Scientific Reports</i> , 2020, 10, 15980.	3.3	12
21	Chloroplast genome data of <i>Luffa acutangula</i> and <i>Luffa aegyptiaca</i> and their phylogenetic relationships. <i>Data in Brief</i> , 2020, 33, 106470.	1.0	5
22	The complete mitochondrial genome of <i>Luffa acutangula</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 3208-3209.	0.4	2
23	Transcriptome analyses reveal the synergistic effects of feeding and eyestalk ablation on ovarian maturation in black tiger shrimp. <i>Scientific Reports</i> , 2020, 10, 3239.	3.3	16
24	A Novel Full-Length Transcriptome Resource for Black Tiger Shrimp (<i>Penaeus monodon</i>) Developed Using Isoform Sequencing (Iso-Seq). <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	21
25	The BPM 24 Rubber Tree Genome, Organellar Genomes and Synteny Within the Family Euphorbiaceae. <i>Compendium of Plant Genomes</i> , 2020, , 55-66.	0.5	3
26	Development of Molecular Markers in <i>Hevea brasiliensis</i> for Marker-Assisted Breeding. <i>Compendium of Plant Genomes</i> , 2020, , 67-79.	0.5	7
27	Optimization of high molecular weight DNA extraction methods in shrimp for a long-read sequencing platform. <i>PeerJ</i> , 2020, 8, e10340.	2.0	15
28	Differential expression between drought-tolerant and drought-sensitive sugarcane under mild and moderate water stress as revealed by a comparative analysis of leaf transcriptome. <i>PeerJ</i> , 2020, 8, e9608.	2.0	22
29	Genome-wide association mapping of virulence gene in rice blast fungus <i>Magnaporthe oryzae</i> using a genotyping by sequencing approach. <i>Genomics</i> , 2019, 111, 661-668.	2.9	25
30	Heat-induced shift in coral microbiome reveals several members of the Rhodobacteraceae family as indicator species for thermal stress in <i>Porites lutea</i> . <i>MicrobiologyOpen</i> , 2019, 8, e935.	3.0	76
31	Dynamics of coral-associated microbiomes during a thermal bleaching event. <i>MicrobiologyOpen</i> , 2018, 7, e00604.	3.0	41
32	Development of a Novel Reference Transcriptome for Scleractinian Coral <i>Porites lutea</i> Using Single-Molecule Long-Read Isoform Sequencing (Iso-Seq). <i>Frontiers in Marine Science</i> , 2018, 5, .	2.5	7
33	Uncovering full-length transcript isoforms of sugarcane cultivar Khon Kaen 3 using single-molecule long-read sequencing. <i>PeerJ</i> , 2018, 6, e5818.	2.0	21
34	Transcriptome analysis of oil palm inflorescences revealed candidate genes for an auxin signaling pathway involved in parthenocarpy. <i>PeerJ</i> , 2018, 6, e5975.	2.0	7
35	De novo hybrid assembly of the rubber tree genome reveals evidence of paleotetraploidy in <i>Hevea</i> species. <i>Scientific Reports</i> , 2017, 7, 41457.	3.3	95
36	High resolution profiling of coral-associated bacterial communities using full-length 16S rRNA sequence data from PacBio SMRT sequencing system. <i>Scientific Reports</i> , 2017, 7, 2774.	3.3	106

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37	The two chromosomes of the mitochondrial genome of a sugarcane cultivar: assembly and recombination analysis using long PacBio reads. <i>Scientific Reports</i> , 2016, 6, 31533.	3.3	55
38	Effects of methylation-sensitive enzymes on the enrichment of genic SNPs and the degree of genome complexity reduction in a two-enzyme genotyping-by-sequencing (GBS) approach: a case study in oil palm (<i>Elaeis guineensis</i>). <i>Molecular Breeding</i> , 2016, 36, 154.	2.1	35
39	Genome-wide SNP discovery and identification of QTL associated with agronomic traits in oil palm using genotyping-by-sequencing (GBS). <i>Genomics</i> , 2015, 105, 288-295.	2.9	132
40	Construction of a high-density integrated genetic linkage map of rubber tree (<i>Hevea brasiliensis</i>) using genotyping-by-sequencing (GBS). <i>Frontiers in Plant Science</i> , 2015, 6, 367.	3.6	102
41	Critical Function of a <i>Chlamydomonas reinhardtii</i> Putative Polyphosphate Polymerase Subunit during Nutrient Deprivation. <i>Plant Cell</i> , 2014, 26, 4214-4229.	6.6	72
42	Large-Scale SNP Discovery through RNA Sequencing and SNP Genotyping by Targeted Enrichment Sequencing in Cassava (<i>Manihot esculenta</i> Crantz). <i>PLoS ONE</i> , 2014, 9, e116028.	2.5	58
43	Development and characterization of single nucleotide polymorphism markers from 454 transcriptome sequences in oil palm (<i>Elaeis guineensis</i>). <i>Plant Breeding</i> , 2013, 132, 711-717.	1.9	12
44	Tiered Regulation of Sulfur Deprivation Responses in <i>Chlamydomonas reinhardtii</i> and Identification of an Associated Regulatory Factor. <i>Plant Physiology</i> , 2013, 162, 195-211.	4.8	34
45	Development of genomic-derived simple sequence repeat markers in <i>Hevea brasiliensis</i> from 454 genome shotgun sequences. <i>Plant Breeding</i> , 2012, 131, 555-562.	1.9	13
46	Reverse genetics in <i>Chlamydomonas</i> : a platform for isolating insertional mutants. <i>Plant Methods</i> , 2011, 7, 24.	4.3	87
47	Single nucleotide polymorphism marker development in the rubber tree, <i>Hevea brasiliensis</i> (Euphorbiaceae). <i>American Journal of Botany</i> , 2011, 98, e337-8.	1.7	39
48	Identification and Regulation of Plasma Membrane Sulfate Transporters in <i>Chlamydomonas</i> . <i>Plant Physiology</i> , 2010, 153, 1653-1668.	4.8	90
49	Genetic Interactions Between Regulators of <i>Chlamydomonas</i> Phosphorus and Sulfur Deprivation Responses. <i>Genetics</i> , 2009, 181, 889-905.	2.9	53
50	Responses to Macronutrient Deprivation. , 2009, , 307-348.		2
51	The Central Role of a SNRK2 Kinase in Sulfur Deprivation Responses. <i>Plant Physiology</i> , 2008, 147, 216-227.	4.8	70
52	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	12.6	2,354
53	Insights into the acclimation of <i>Chlamydomonas reinhardtii</i> to sulfur deprivation. <i>Photosynthesis Research</i> , 2005, 86, 475-489.	2.9	63