

Charles A Hefer

List of Publications by Year in descending order

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31
papers

2,078
citations

394421

19
h-index

454955

30
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34
all docs

34
docs citations

34
times ranked

3409
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725
2	De novo assembled expressed gene catalog of a fast-growing <i>Eucalyptus</i> tree produced by Illumina mRNA-Seq. <i>BMC Genomics</i> , 2010, 11, 681.	2.8	150
3	The <i>Eucalyptus</i> terpene synthase gene family. <i>BMC Genomics</i> , 2015, 16, 450.	2.8	125
4	Recent Y chromosome divergence despite ancient origin of dioecy in poplars (<i>Populus</i>). <i>Molecular Ecology</i> , 2015, 24, 3243-3256.	3.9	121
5	Genome-wide analysis of the lignin toolbox of <i>Eucalyptus grandis</i> . <i>New Phytologist</i> , 2015, 206, 1297-1313.	7.3	113
6	The <i>Eucalyptus grandis</i> <i>R2R3</i> MYB transcription factor family: evidence for woody growth-related evolution and function. <i>New Phytologist</i> , 2015, 206, 1364-1377.	7.3	107
7	Whole plastome sequencing reveals deep plastid divergence and cytonuclear discordance between closely related balsam poplars, <i>Populus balsamifera</i> and <i>P. trichocarpa</i> (<i>Salicaceae</i>). <i>New Phytologist</i> , 2014, 204, 693-703.	7.3	105
8	Genomic and functional approaches reveal a case of adaptive introgression from <i>Populus balsamifera</i> (balsam poplar) in <i>P. trichocarpa</i> (black cottonwood). <i>Molecular Ecology</i> , 2016, 25, 2427-2442.	3.9	85
9	Structural, evolutionary and functional analysis of the <i>NAC</i> domain protein family in <i>Eucalyptus</i> . <i>New Phytologist</i> , 2015, 206, 1337-1350.	7.3	69
10	The floral transcriptome of <i>Eucalyptus grandis</i> . <i>New Phytologist</i> , 2015, 206, 1406-1422.	7.3	61
11	Comparative interrogation of the developing xylem transcriptomes of two wood-forming species: <i>Populus trichocarpa</i> and <i>Eucalyptus grandis</i> . <i>New Phytologist</i> , 2015, 206, 1391-1405.	7.3	47
12	Genomic population structure and prevalence of copy number variations in South African Nguni cattle. <i>BMC Genomics</i> , 2015, 16, 894.	2.8	46
13	Introgression from <i>Populus balsamifera</i> underlies adaptively significant variation and range boundaries in <i>P. trichocarpa</i> . <i>New Phytologist</i> , 2018, 217, 416-427.	7.3	36
14	Genetic dissection of growth, wood basic density and gene expression in interspecific backcrosses of <i>Eucalyptus grandis</i> and <i>E. urophylla</i> . <i>BMC Genetics</i> , 2012, 13, 60.	2.7	31
15	Investigating the molecular underpinnings underlying morphology and changes in carbon partitioning during tension wood formation in <i>Eucalyptus</i> . <i>New Phytologist</i> , 2015, 206, 1351-1363.	7.3	27
16	Functional network analysis of genes differentially expressed during xylogenesis in woody <i>Arabidopsis</i> plants. <i>Plant Journal</i> , 2016, 86, 376-390.	5.7	27
17	The <i>Eucalyptus grandis</i> Genome Project: Genome and transcriptome resources for comparative analysis of woody plant biology. <i>BMC Proceedings</i> , 2011, 5, .	1.6	25
18	Scale and direction of adaptive introgression between black cottonwood (<i>Populus</i>) and <i>Eucalyptus</i> . <i>Evolution</i> , 2018, 72, 1050-1062.	3.9	25

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19	Altering carbon allocation in hybrid poplar (<i>Populus alba</i> – <i>P. grandidentata</i>) impacts cell wall growth and development. <i>Plant Biotechnology Journal</i> , 2017, 15, 865-878.	8.3	24
20	The transcriptional landscape of insect galls: psyllid (Hemiptera) gall formation in Hawaiian <i>Metrosideros polymorpha</i> (Myrtaceae). <i>BMC Genomics</i> , 2015, 16, 943.	2.8	23
21	Comparative analysis of plant carbohydrate active enzymes and their role in xylogenesis. <i>BMC Genomics</i> , 2015, 16, 402.	2.8	23
22	The Eucalyptus genome integrative explorer (EucGenIE): a resource for Eucalyptus genomics and transcriptomics. <i>BMC Proceedings</i> , 2011, 5, .	1.6	18
23	Bin mapping of tomato diversity array (DART) markers to genomic regions of <i>Solanum lycopersicum</i> – <i>Solanum pennellii</i> introgression lines. <i>Theoretical and Applied Genetics</i> , 2012, 124, 947-956.	3.6	18
24	Exploiting Natural Variation to Uncover an Alkene Biosynthetic Enzyme in Poplar. <i>Plant Cell</i> , 2017, 29, 2000-2015.	6.6	17
25	The wool proteome and fibre characteristics of three distinct genetic ovine breeds from Portugal. <i>Journal of Proteomics</i> , 2020, 225, 103853.	2.4	10
26	The complete genome sequence of the nitrile biocatalyst <i>Rhodococcus rhodochrous</i> ATCC BAA-870. <i>BMC Genomics</i> , 2020, 21, 3.	2.8	7
27	Phylogenomic structure of <i>Bacillus anthracis</i> isolates in the Northern Cape Province, South Africa revealed novel single nucleotide polymorphisms. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104146.	2.3	5
28	Genetic dissection of transcript, metabolite, growth and wood property traits in an F2 pseudo-backcross pedigree of <i>Eucalyptus grandis</i> x <i>E. urophylla</i> . <i>BMC Proceedings</i> , 2011, 5, .	1.6	3
29	Defining the QTL associated with chill requirement during endodormancy in <i>Malus domestica</i> Borkh. <i>Euphytica</i> , 2020, 216, 1.	1.2	2
30	Proteomic Profile of <i>M. Longissimus Thoracis</i> from Commercial Lambs Reared in Different Forage Systems. <i>Foods</i> , 2022, 11, 1419.	4.3	1
31	Insights in Human Hair Curvature by Proteome Analysis of Two Distinct Hair Shapes.. <i>Journal of Cosmetic Science</i> , 2021, 72, 249-267.	0.1	0