Marc W Crepeau

List of Publications by Citations

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23 1,803 18 23 g-index

23 2,420 5.5 4.04 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
23	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014 , 15, R59	18.3	347
22	Population Genomics of sub-saharan Drosophila melanogaster: African diversity and non-African admixture. <i>PLoS Genetics</i> , 2012 , 8, e1003080	6	225
21	Sequencing and assembly of the 22-gb loblolly pine genome. <i>Genetics</i> , 2014 , 196, 875-90	4	211
20	The Drosophila genome nexus: a population genomic resource of 623 Drosophila melanogaster genomes, including 197 from a single ancestral range population. <i>Genetics</i> , 2015 , 199, 1229-41	4	170
19	Unique features of the loblolly pine (Pinus taeda L.) megagenome revealed through sequence annotation. <i>Genetics</i> , 2014 , 196, 891-909	4	146
18	The walnut (Juglans regia) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. <i>Plant Journal</i> , 2016 , 87, 507-32	6.9	127
17	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016 , 204, 1613-1626	4	119
16	First Draft Assembly and Annotation of the Genome of a California Endemic Oak N∄ (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3485-3495	3.2	57
15	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3157-3167	3.2	55
14	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. <i>GigaScience</i> , 2017 , 6, 1-4	7.6	44
13	Insights into the loblolly pine genome: characterization of BAC and fosmid sequences. <i>PLoS ONE</i> , 2013 , 8, e72439	3.7	41
12	Modification of distinct aspects of photomorphogenesis via targeted expression of mammalian biliverdin reductase in transgenic Arabidopsis plants. <i>Plant Physiology</i> , 1999 , 121, 629-39	6.6	40
11	Circumventing heterozygosity: sequencing the amplified genome of a single haploid Drosophila melanogaster embryo. <i>Genetics</i> , 2011 , 188, 239-46	4	38
10	A new genomic tool for walnut (Juglans regia L.): development and validation of the high-density Axiom (J. regia 700K SNP genotyping array. <i>Plant Biotechnology Journal</i> , 2019 , 17, 1027-1036	11.6	34
9	Genomic architecture of complex traits in loblolly pine. New Phytologist, 2019, 221, 1789-1801	9.8	32
8	Genomic Variation Among and Within Six Species. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 2153-2165	3.2	25
7	Combination of multipoint maximum likelihood (MML) and regression mapping algorithms to construct a high-density genetic linkage map for loblolly pine (Pinus taeda L.). <i>Tree Genetics and Genomes</i> , 2013 , 9, 1529-1535	2.1	19

LIST OF PUBLICATIONS

6	Development of a highly efficient Axiom 170 K SNP array for Pyrus and evaluation for high-density mapping and germplasm characterization. <i>BMC Genomics</i> , 2019 , 20, 331	4.5	18
5	Genomic basis of white pine blister rust quantitative disease resistance and its relationship with qualitative resistance. <i>Plant Journal</i> , 2020 , 104, 365-376	6.9	18
4	Biliverdin reductase-induced phytochrome chromophore deficiency in transgenic tobacco. <i>Plant Physiology</i> , 2001 , 125, 266-77	6.6	14
3	From Pine Cones to Read Clouds: Rescaffolding the Megagenome of Sugar Pine (). <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 1563-1568	3.2	12
2	Dissecting the Polygenic Basis of Cold Adaptation Using Genome-Wide Association of Traits and Environmental Data in Douglas-fir. <i>Genes</i> , 2021 , 12,	4.2	6
1	Histone deacetylase inhibitor treatment promotes spontaneous caregiving behaviour in non-aggressive virgin male mice. <i>Journal of Neuroendocrinology</i> , 2019 , 31, e12734	3.8	5