

Marc W Crepeau

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

2,692
citations

393982

19
h-index

642321

23
g-index

23
all docs

23
docs citations

23
times ranked

2998
citing authors

#	ARTICLE	IF	CITATIONS
1	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014, 15, R59.	13.9	424
2	Population Genomics of Sub-Saharan <i>Drosophila melanogaster</i> : African Diversity and Non-African Admixture. <i>PLoS Genetics</i> , 2012, 8, e1003080.	1.5	318
3	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. <i>Genetics</i> , 2014, 196, 875-890.	1.2	286
4	The <i>Drosophila</i> Genome Nexus: A Population Genomic Resource of 623 <i>Drosophila melanogaster</i> Genomes, Including 197 from a Single Ancestral Range Population. <i>Genetics</i> , 2015, 199, 1229-1241.	1.2	273
5	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. <i>Plant Journal</i> , 2016, 87, 507-532.	2.8	233
6	Unique Features of the Loblolly Pine (<i>Pinus taeda</i> L.) Megagenome Revealed Through Sequence Annotation. <i>Genetics</i> , 2014, 196, 891-909.	1.2	207
7	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016, 204, 1613-1626.	1.2	169
8	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3157-3167.	0.8	103
9	First Draft Assembly and Annotation of the Genome of a California Endemic Oak (<i>Quercus lobata</i> (Fagaceae)). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3485-3495.	0.8	95
10	A new genomic tool for walnut (<i>Juglans regia</i> L.): development and validation of the high-density Axiom [®] , 70K SNP genotyping array. <i>Plant Biotechnology Journal</i> , 2019, 17, 1027-1036.	4.1	79
11	Genomic Variation Among and Within Six <i>Juglans</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2153-2165.	0.8	73
12	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. <i>GigaScience</i> , 2017, 6, 1-4.	3.3	71
13	Genomic architecture of complex traits in loblolly pine. <i>New Phytologist</i> , 2019, 221, 1789-1801.	3.5	60
14	Circumventing Heterozygosity: Sequencing the Amplified Genome of a Single Haploid <i>Drosophila melanogaster</i> Embryo. <i>Genetics</i> , 2011, 188, 239-246.	1.2	51
15	Modification of Distinct Aspects of Photomorphogenesis via Targeted Expression of Mammalian Biliverdin Reductase in Transgenic Arabidopsis Plants. <i>Plant Physiology</i> , 1999, 121, 629-640.	2.3	47
16	Insights into the Loblolly Pine Genome: Characterization of BAC and Fosmid Sequences. <i>PLoS ONE</i> , 2013, 8, e72439.	1.1	46
17	Development of a highly efficient Axiom [®] , 70 K SNP array for <i>Pyrus</i> and evaluation for high-density mapping and germplasm characterization. <i>BMC Genomics</i> , 2019, 20, 331.	1.2	40
18	Genomic basis of white pine blister rust quantitative disease resistance and its relationship with qualitative resistance. <i>Plant Journal</i> , 2020, 104, 365-376.	2.8	32

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19	Combination of multipoint maximum likelihood (MML) and regression mapping algorithms to construct a high-density genetic linkage map for loblolly pine (<i>Pinus taeda</i> L.). <i>Tree Genetics and Genomes</i> , 2013, 9, 1529-1535.	0.6	23
20	Biliverdin Reductase-Induced Phytochrome Chromophore Deficiency in Transgenic Tobacco. <i>Plant Physiology</i> , 2001, 125, 266-277.	2.3	20
21	From Pine Cones to Read Clouds: Rescaffolding the Megagenome of Sugar Pine (<i>Pinus lambertiana</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1563-1568.	0.8	19
22	Dissecting the Polygenic Basis of Cold Adaptation Using Genome-Wide Association of Traits and Environmental Data in Douglas-fir. <i>Genes</i> , 2021, 12, 110.	1.0	14
23	Histone deacetylase inhibitor treatment promotes spontaneous caregiving behaviour in non-aggressive virgin male mice. <i>Journal of Neuroendocrinology</i> , 2019, 31, e12734.	1.2	9