

Marc W Crepeau

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

23
papers

1,803
citations

18
h-index

23
g-index

23
ext. papers

2,420
ext. citations

5.5
avg, IF

4.04
L-index

#	Paper	IF	Citations
23	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
22	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
21	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
20	Development of a highly efficient Axiom 70 K SNP array for Pyrus and evaluation for high-density mapping and germplasm characterization. <i>BMC Genomics</i> , 2019 , 20, 331	4.5	18
19	Genomic architecture of complex traits in loblolly pine. <i>New Phytologist</i> , 2019 , 221, 1789-1801	9.8	32
18	A new genomic tool for walnut (<i>Juglans regia</i> L.): development and validation of the high-density Axiom \square . <i>regia</i> 700K SNP genotyping array. <i>Plant Biotechnology Journal</i> , 2019 , 17, 1027-1036	11.6	34
17	Genomic Variation Among and Within Six Species. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 2153-2165	3.2	25
16	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
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	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016 , 204, 1613-1626	4	119
12	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, 507-32	6.9	127
11	First Draft Assembly and Annotation of the Genome of a California Endemic Oak N \bar{B} (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3485-3495	3.2	57
10	The Drosophila 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, 1229-41	4	170
9	Unique features of the loblolly pine (<i>Pinus taeda</i> L.) megagenome revealed through sequence annotation. <i>Genetics</i> , 2014 , 196, 891-909	4	146
8	Sequencing and assembly of the 22-gb loblolly pine genome. <i>Genetics</i> , 2014 , 196, 875-90	4	211
7	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014 , 15, R59	18.3	347

6	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	2.1	19
5	Insights into the loblolly pine genome: characterization of BAC and fosmid sequences. <i>PLoS ONE</i> , 2013 , 8, e72439	3.7	41
4	Population Genomics of sub-saharan <i>Drosophila melanogaster</i> : African diversity and non-African admixture. <i>PLoS Genetics</i> , 2012 , 8, e1003080	6	225
3	Circumventing heterozygosity: sequencing the amplified genome of a single haploid <i>Drosophila melanogaster</i> embryo. <i>Genetics</i> , 2011 , 188, 239-46	4	38
2	Biliverdin reductase-induced phytochrome chromophore deficiency in transgenic tobacco. <i>Plant Physiology</i> , 2001 , 125, 266-77	6.6	14
1	Modification of distinct aspects of photomorphogenesis via targeted expression of mammalian biliverdin reductase in transgenic <i>Arabidopsis</i> plants. <i>Plant Physiology</i> , 1999 , 121, 629-39	6.6	40