## Marc W Crepeau

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Dissecting the Polygenic Basis of Cold Adaptation Using Genome-Wide Association of Traits and Environmental Data in Douglas-fir. Genes, 2021, 12, 110.	2.4	14
2	Genomic basis of white pine blister rust quantitative disease resistance and its relationship with qualitative resistance. Plant Journal, 2020, 104, 365-376.	5.7	32
3	Histone deacetylase inhibitor treatment promotes spontaneous caregiving behaviour in nonâ€aggressive virgin male mice. Journal of Neuroendocrinology, 2019, 31, e12734.	2.6	9
4	Development of a highly efficient Axiomâ"¢ 70 K SNP array for Pyrus and evaluation for high-density mapping and germplasm characterization. BMC Genomics, 2019, 20, 331.	2.8	40
5	Genomic architecture of complex traits in loblolly pine. New Phytologist, 2019, 221, 1789-1801.	7.3	60
6	A new genomic tool for walnut ( Juglans regia L.): development and validation of the highâ€density Axiomâ"¢ J.Âregia 700K SNP genotyping array. Plant Biotechnology Journal, 2019, 17, 1027-1036.	8.3	79
7	Genomic Variation Among and Within Six <i>Juglans</i> Species. G3: Genes, Genomes, Genetics, 2018, 8, 2153-2165.	1.8	73
8	From Pine Cones to Read Clouds: Rescaffolding the Megagenome of Sugar Pine (Pinus lambertiana). G3: Genes, Genomes, Genetics, 2017, 7, 1563-1568.	1.8	19
9	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. G3: Genes, Genomes, Genetics, 2017, 7, 3157-3167.	1.8	103
10	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. GigaScience, 2017, 6, 1-4.	6.4	71
11	First Draft Assembly and Annotation of the Genome of a California Endemic Oak <i>Quercus lobata</i> Née (Fagaceae). G3: Genes, Genomes, Genetics, 2016, 6, 3485-3495.	1.8	95
12	Sequence of the Sugar Pine Megagenome. Genetics, 2016, 204, 1613-1626.	2.9	169
13	The walnut ( <i>Juglans regia</i> ) genome sequence reveals diversity in genes coding for the biosynthesis of nonâ€structural polyphenols. Plant Journal, 2016, 87, 507-532.	5.7	233
14	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. Genetics, 2015, 199, 1229-1241.	2.9	273
15	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. Genetics, 2014, 196, 875-890.	2.9	286
16	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. Genome Biology, 2014, 15, R59.	9.6	424
17	Unique Features of the Loblolly Pine ( <i>Pinus taeda</i> L.) Megagenome Revealed Through Sequence Annotation. Genetics, 2014, 196, 891-909.	2.9	207
18	Combination of multipoint maximum likelihood (MML) and regression mapping algorithms to construct a high-density genetic linkage map for loblolly pine (Pinus taeda L.). Tree Genetics and Genomes, 2013, 9, 1529-1535.	1.6	23

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#	ARTICLE	IF	CITATIONS
19	Insights into the Loblolly Pine Genome: Characterization of BAC and Fosmid Sequences. PLoS ONE, 2013, 8, e72439.	2.5	46
20	Population Genomics of Sub-Saharan Drosophila melanogaster: African Diversity and Non-African Admixture. PLoS Genetics, 2012, 8, e1003080.	3.5	318
21	Circumventing Heterozygosity: Sequencing the Amplified Genome of a Single Haploid <i>Drosophila melanogaster</i> Embryo. Genetics, 2011, 188, 239-246.	2.9	51
22	Biliverdin Reductase-Induced Phytochrome Chromophore Deficiency in Transgenic Tobacco. Plant Physiology, 2001, 125, 266-277.	4.8	20
23	Modification of Distinct Aspects of Photomorphogenesis via Targeted Expression of Mammalian Biliverdin Reductase in Transgenic Arabidopsis Plants. Plant Physiology, 1999, 121, 629-640.	4.8	47