Kristian A Stevens

List of Publications by Year
in descending order

16 papers	2,400 citations	516710 16 h-index	940533 16 g-index
16 all docs	16 docs citations	16 times ranked	2689 citing authors

#	Article	IF	Citations
1	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. Genome Biology, 2014, 15, R59.	9.6	424
2	Population Genomics of Sub-Saharan Drosophila melanogaster: African Diversity and Non-African Admixture. PLoS Genetics, 2012, 8, e1003080.	3.5	318
3	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. Genetics, 2014, 196, 875-890.	2.9	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. Genetics, 2015, 199, 1229-1241.	2.9	273
5	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of non‐structural polyphenols. Plant Journal, 2016, 87, 507-532.	5.7	233
6	Unique Features of the Loblolly Pine (<i>Pinus taeda</i> L.) Megagenome Revealed Through Sequence Annotation. Genetics, 2014, 196, 891-909.	2.9	207
7	Sequence of the Sugar Pine Megagenome. Genetics, 2016, 204, 1613-1626.	2.9	169
8	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. G3: Genes, Genomes, Genetics, 2017, 7, 3157-3167.	1.8	103
9	A new genomic tool for walnut (Juglans regia L.): development and validation of the high‐density Axiom™ J.Âregia 700K SNP genotyping array. Plant Biotechnology Journal, 2019, 17, 1027-1036.	8.3	79
10	Genomic Variation Among and Within Six <i>Juglans</i> Species. G3: Genes, Genomes, Genetics, 2018, 8, 2153-2165.	1.8	73
11	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. GigaScience, 2017, 6, 1-4.	6.4	71
12	Assessing the Gene Content of the Megagenome: Sugar Pine (<i>Pinus lambertiana</i>). G3: Genes, Genomes, Genetics, 2016, 6, 3787-3802.	1.8	51
13	Insights into the Loblolly Pine Genome: Characterization of BAC and Fosmid Sequences. PLoS ONE, 2013, 8, e72439.	2.5	46
14	Comparative genomics of six <i>Juglans</i> species reveals disease‐associated gene family contractions. Plant Journal, 2020, 102, 410-423.	5.7	25
15	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
16	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