

# Kristian A Stevens

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12017746/publications.pdf>

Version: 2024-02-01

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	Comparative genomics of six <i>Juglans</i> species reveals disease-associated gene family contractions. <i>Plant Journal</i> , 2020, 102, 410-423.	5.7	25
2	A new genomic tool for walnut ( <i>Juglans regia</i> L.): development and validation of the high-density Axioma <sup>®</sup> J. <i>Regia</i> 700K SNP genotyping array. <i>Plant Biotechnology Journal</i> , 2019, 17, 1027-1036.	8.3	79
3	Genomic Variation Among and Within Six <i>Juglans</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2153-2165.	1.8	73
4	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.	1.8	19
5	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3157-3167.	1.8	103
6	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. <i>GigaScience</i> , 2017, 6, 1-4.	6.4	71
7	Assessing the Gene Content of the Megagenome: Sugar Pine ( <i>Pinus lambertiana</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3787-3802.	1.8	51
8	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016, 204, 1613-1626.	2.9	169
9	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.	5.7	233
10	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.	2.9	273
11	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. <i>Genetics</i> , 2014, 196, 875-890.	2.9	286
12	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014, 15, R59.	9.6	424
13	Unique Features of the Loblolly Pine ( <i>Pinus taeda</i> L.) Megagenome Revealed Through Sequence Annotation. <i>Genetics</i> , 2014, 196, 891-909.	2.9	207
14	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.	1.6	23
15	Insights into the Loblolly Pine Genome: Characterization of BAC and Fosmid Sequences. <i>PLoS ONE</i> , 2013, 8, e72439.	2.5	46
16	Population Genomics of Sub-Saharan <i>Drosophila melanogaster</i> : African Diversity and Non-African Admixture. <i>PLoS Genetics</i> , 2012, 8, e1003080.	3.5	318