Daniela Puiu

List of Publications by Year
in descending order

29 papers	5,411 citations	304368 22 h-index	454577 30 g-index
31 all docs	31 docs citations	31 times ranked	8848 citing authors

#	Article	IF	Citations
1	Genomeâ€wide association identifies candidate genes for drought tolerance in coast redwood and giant sequoia. Plant Journal, 2022, 109, 7-22.	2.8	17
2	Assembled and annotated 26.5 Gbp coast redwood genome: a resource for estimating evolutionary adaptive potential and investigating hexaploid origin. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	28
3	A reference-quality, fully annotated genome from a Puerto Rican individual. Genetics, 2022, 220, .	1.2	7
4	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. Nature Communications, 2022, 13, 2047.	5.8	30
5	A bioinformatics pipeline for estimating mitochondrial DNA copy number and heteroplasmy levels from whole genome sequencing data. NAR Genomics and Bioinformatics, 2022, 4, lqac034.	1.5	12
6	Dissecting the Polygenic Basis of Cold Adaptation Using Genome-Wide Association of Traits and Environmental Data in Douglas-fir. Genes, 2021, 12, 110.	1.0	14
7	Genomic basis of white pine blister rust quantitative disease resistance and its relationship with qualitative resistance. Plant Journal, 2020, 104, 365-376.	2.8	32
8	A Reference Genome Sequence for Giant Sequoia. G3: Genes, Genomes, Genetics, 2020, 10, 3907-3919.	0.8	67
9	Chromosome-Scale Assembly of the Bread Wheat Genome Reveals Thousands of Additional Gene Copies. Genetics, 2020, 216, 599-608.	1.2	34
10	High-quality chromosome-scale assembly of the walnut (Juglans regia L.) reference genome. GigaScience, 2020, 9, .	3.3	83
11	Assembly and annotation of an Ashkenazi human reference genome. Genome Biology, 2020, 21, 129.	3.8	42
12	The genome of the American groundhog, Marmota monax. F1000Research, 2020, 9, 1137.	0.8	3
13	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. Nature Genetics, 2019, 51, 30-35.	9.4	276
14	Genomic architecture of complex traits in loblolly pine. New Phytologist, 2019, 221, 1789-1801.	3.5	60
15	Hybrid assembly of the large and highly repetitive genome of <i>Aegilops tauschii</i>, a progenitor of bread wheat, with the MaSuRCA mega-reads algorithm. Genome Research, 2017, 27, 787-792.	2.4	382
16	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. G3: Genes, Genomes, Genetics, 2017, 7, 3157-3167.	0.8	103
17	Genome sequence of the progenitor of the wheat D genome Aegilops tauschii. Nature, 2017, 551, 498-502.	13.7	563
18	The first near-complete assembly of the hexaploid bread wheat genome, Triticum aestivum. GigaScience, 2017, 6, 1-7.	3.3	224

#	Article	IF	Citations
19	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. GigaScience, 2017, 6, 1-4.	3.3	71
20	First Draft Assembly and Annotation of the Genome of a California Endemic Oak *Quercus lobata* Née (Fagaceae). G3: Genes, Genomes, Genetics, 2016, 6, 3485-3495.	0.8	95
21	Sequence of the Sugar Pine Megagenome. Genetics, 2016, 204, 1613-1626.	1.2	169
22	The walnut (*Juglans regia*) genome sequence reveals diversity in genes coding for the biosynthesis of non‐structural polyphenols. Plant Journal, 2016, 87, 507-532.	2.8	233
23	A First Insight into the Genome of the Filter-Feeder Mussel Mytilus galloprovincialis. PLoS ONE, 2016, 11, e0151561.	1.1	124
24	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	3.8	330
25	Genomic signatures of evolutionary transitions from solitary to group living. Science, 2015, 348, 1139-1143.	6.0	357
26	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. Genetics, 2014, 196, 875-890.	1.2	286
27	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. Genome Biology, 2014, 15, R59.	13.9	424
28	Unique Features of the Loblolly Pine (*Pinus taeda* L.) Megagenome Revealed Through Sequence Annotation. Genetics, 2014, 196, 891-909.	1.2	207
29	The MaSuRCA genome assembler. Bioinformatics, 2013, 29, 2669-2677.	1.8	1,127