

Daniela Puiu

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.

30
papers

3,404
citations

20
h-index

31
g-index

31
ext. papers

4,716
ext. citations

10.3
avg, IF

4.79
L-index

#	Paper	IF	Citations
30	Assembled and annotated 26.5 Gbp coast redwood genome: a resource for estimating evolutionary adaptive potential and investigating hexaploid origin.. <i>G3: Genes, Genomes, Genetics</i> , 2022 , 12,	3.2	4
29	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks.. <i>Nature Communications</i> , 2022 , 13, 2047	17.4	2
28	A bioinformatics pipeline for estimating mitochondrial DNA copy number and heteroplasmy levels from whole genome sequencing data.. <i>NAR Genomics and Bioinformatics</i> , 2022 , 4, lqac034	3.7	0
27	A reference-quality, fully annotated genome from a Puerto Rican individual.. <i>Genetics</i> , 2021 ,	4	2
26	Genome-wide association identifies candidate genes for drought tolerance in coast redwood and giant sequoia. <i>Plant Journal</i> , 2021 ,	6.9	2
25	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
24	High-quality chromosome-scale assembly of the walnut (<i>Juglans regia</i> L.) reference genome. <i>GigaScience</i> , 2020 , 9,	7.6	33
23	Assembly and annotation of an Ashkenazi human reference genome. <i>Genome Biology</i> , 2020 , 21, 129	18.3	20
22	The genome of the American groundhog,. <i>F1000Research</i> , 2020 , 9, 1137	3.6	0
21	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
20	A Reference Genome Sequence for Giant Sequoia. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3907-3919	3.2	22
19	Chromosome-Scale Assembly of the Bread Wheat Genome Reveals Thousands of Additional Gene Copies. <i>Genetics</i> , 2020 , 216, 599-608	4	17
18	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. <i>Nature Genetics</i> , 2019 , 51, 30-35	36.3	153
17	Genomic architecture of complex traits in loblolly pine. <i>New Phytologist</i> , 2019 , 221, 1789-1801	9.8	32
16	Hybrid assembly of the large and highly repetitive genome of , a progenitor of bread wheat, with the MaSuRCA mega-reads algorithm. <i>Genome Research</i> , 2017 , 27, 787-792	9.7	208
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	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017 , 551, 498-502	20.4	337

13	The first near-complete assembly of the hexaploid bread wheat genome, <i>Triticum aestivum</i> . <i>GigaScience</i> , 2017 , 6, 1-7	7.6	157
12	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
11	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016 , 204, 1613-1626	4	119
10	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
9	A First Insight into the Genome of the Filter-Feeder Mussel <i>Mytilus galloprovincialis</i> . <i>PLoS ONE</i> , 2016 , 11, e0151561	3.7	90
8	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
7	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015 , 16, 76	18.3	229
6	Social evolution. Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015 , 348, 1139-43	33.3	256
5	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
4	Sequencing and assembly of the 22-gb loblolly pine genome. <i>Genetics</i> , 2014 , 196, 875-90	4	211
3	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014 , 15, R59	18.3	347
2	The MaSuRCA genome assembler. <i>Bioinformatics</i> , 2013 , 29, 2669-77	7.2	703
1	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks		2