

Daniela Puiu

List of Publications by Year in descending order

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Version: 2024-02-01

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	The MaSuRCA genome assembler. <i>Bioinformatics</i> , 2013, 29, 2669-2677.	1.8	1,127
2	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563
3	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014, 15, R59.	13.9	424
4	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. <i>Genome Research</i> , 2017, 27, 787-792.	2.4	382
5	Genomic signatures of evolutionary transitions from solitary to group living. <i>Science</i> , 2015, 348, 1139-1143.	6.0	357
6	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , 2015, 16, 76.	3.8	330
7	Sequencing and Assembly of the 22-Gb Loblolly Pine Genome. <i>Genetics</i> , 2014, 196, 875-890.	1.2	286
8	Assembly of a pan-genome from deep sequencing of 910 humans of African descent. <i>Nature Genetics</i> , 2019, 51, 30-35.	9.4	276
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.	2.8	233
10	The first near-complete assembly of the hexaploid bread wheat genome, <i>Triticum aestivum</i> . <i>GigaScience</i> , 2017, 6, 1-7.	3.3	224
11	Unique Features of the Loblolly Pine (<i>Pinus taeda</i> L.) Megagenome Revealed Through Sequence Annotation. <i>Genetics</i> , 2014, 196, 891-909.	1.2	207
12	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016, 204, 1613-1626.	1.2	169
13	A First Insight into the Genome of the Filter-Feeder Mussel <i>Mytilus galloprovincialis</i> . <i>PLoS ONE</i> , 2016, 11, e0151561.	1.1	124
14	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3157-3167.	0.8	103
15	First Draft Assembly and Annotation of the Genome of a California Endemic Oak <i>Quercus lobata</i> (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3485-3495.	0.8	95
16	High-quality chromosome-scale assembly of the walnut (<i>Juglans regia</i> L.) reference genome. <i>GigaScience</i> , 2020, 9, .	3.3	83
17	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. <i>GigaScience</i> , 2017, 6, 1-4.	3.3	71
18	A Reference Genome Sequence for Giant Sequoia. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3907-3919.	0.8	67

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19	Genomic architecture of complex traits in loblolly pine. <i>New Phytologist</i> , 2019, 221, 1789-1801.	3.5	60
20	Assembly and annotation of an Ashkenazi human reference genome. <i>Genome Biology</i> , 2020, 21, 129.	3.8	42
21	Chromosome-Scale Assembly of the Bread Wheat Genome Reveals Thousands of Additional Gene Copies. <i>Genetics</i> , 2020, 216, 599-608.	1.2	34
22	Genomic basis of white pine blister rust quantitative disease resistance and its relationship with qualitative resistance. <i>Plant Journal</i> , 2020, 104, 365-376.	2.8	32
23	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. <i>Nature Communications</i> , 2022, 13, 2047.	5.8	30
24	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, .	0.8	28
25	Genome-wide association identifies candidate genes for drought tolerance in coast redwood and giant sequoia. <i>Plant Journal</i> , 2022, 109, 7-22.	2.8	17
26	Dissecting the Polygenic Basis of Cold Adaptation Using Genome-Wide Association of Traits and Environmental Data in Douglas-fir. <i>Genes</i> , 2021, 12, 110.	1.0	14
27	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.	1.5	12
28	A reference-quality, fully annotated genome from a Puerto Rican individual. <i>Genetics</i> , 2022, 220, .	1.2	7
29	The genome of the American groundhog, <i>Marmota monax</i> . <i>F1000Research</i> , 2020, 9, 1137.	0.8	3