

Alex Di Genova

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

2,912
citations

471477

17
h-index

501174

28
g-index

33
all docs

33
docs citations

33
times ranked

5749
citing authors

#	ARTICLE	IF	CITATIONS
1	The Atlantic salmon genome provides insights into rediploidization. <i>Nature</i> , 2016, 533, 200-205.	27.8	1,021
2	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015, 43, W589-W598.	14.5	682
3	Construction of Reference Chromosome-Scale Pseudomolecules for Potato: Integrating the Potato Genome with Genetic and Physical Maps. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2031-2047.	1.8	244
4	Genome-wide association analysis reveals loci associated with resistance against <i>Piscirickettsia salmonis</i> in two Atlantic salmon (<i>Salmo salar</i> L.) chromosomes. <i>BMC Genomics</i> , 2015, 16, 854.	2.8	120
5	Whole genome comparison between table and wine grapes reveals a comprehensive catalog of structural variants. <i>BMC Plant Biology</i> , 2014, 14, 7.	3.6	115
6	Genome wide association study for resistance to <i>Caligus rogercresseyi</i> in Atlantic salmon (<i>Salmo</i>) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50	3.5	95
7	The bioleaching potential of a bacterial consortium. <i>Bioresource Technology</i> , 2016, 218, 659-666.	9.6	63
8	Genomic variation underlying complex life-history traits revealed by genome sequencing in Chinook salmon. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180935.	2.6	62
9	Comparing genomic signatures of domestication in two Atlantic salmon (<i>Salmo salar</i> L.) populations with different geographical origins. <i>Evolutionary Applications</i> , 2019, 12, 137-156.	3.1	58
10	Identification of two putative reference genes from grapevine suitable for gene expression analysis in berry and related tissues derived from RNA-Seq data. <i>BMC Genomics</i> , 2013, 14, 878.	2.8	50
11	A new genome of <i>Acidithiobacillus thiooxidans</i> provides insights into adaptation to a bioleaching environment. <i>Research in Microbiology</i> , 2014, 165, 743-752.	2.1	48
12	Efficient hybrid de novo assembly of human genomes with WENGAN. <i>Nature Biotechnology</i> , 2021, 39, 422-430.	17.5	47
13	Reconstruction of the microalga <i>Nannochloropsis salina</i> genome-scale metabolic model with applications to lipid production. <i>BMC Systems Biology</i> , 2017, 11, 66.	3.0	41
14	The transposable element-rich genome of the cereal pest <i>Sitophilus oryzae</i> . <i>BMC Biology</i> , 2021, 19, 241.	3.8	40
15	Transcriptome sequencing of <i>Prunus</i> sp. rootstocks roots to identify candidate genes involved in the response to root hypoxia. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	34
16	SalmonDB: a bioinformatics resource for <i>Salmo salar</i> and <i>Oncorhynchus mykiss</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar050-bar050.	3.0	28
17	Genome wide identification of <i>Acidithiobacillus ferrooxidans</i> (ATCC 23270) transcription factors and comparative analysis of ArsR and MerR metal regulators. <i>BioMetals</i> , 2012, 25, 75-93.	4.1	21
18	Transcriptome profiling of grapevine seedless segregants during berry development reveals candidate genes associated with berry weight. <i>BMC Plant Biology</i> , 2016, 16, 104.	3.6	18

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19	Identification of SNPs and InDels associated with berry size in table grapes integrating genetic and transcriptomic approaches. <i>BMC Plant Biology</i> , 2020, 20, 365.	3.6	18
20	Development of a small panel of SNPs to infer ancestry in Chileans that distinguishes Aymara and Mapuche components. <i>Biological Research</i> , 2020, 53, 15.	3.4	18
21	Cdk5 regulates Rap1 activity. <i>Neurochemistry International</i> , 2013, 62, 848-853.	3.8	15
22	RNA-Seq analysis and transcriptome assembly of raspberry fruit (<i>Rubus idaeus</i> 'Heritage') revealed several candidate genes involved in fruit development and ripening. <i>Scientia Horticulturae</i> , 2019, 254, 26-34.	3.6	15
23	Bioinformatic survey for new physiological substrates of Cyclin-dependent kinase 5. <i>Genomics</i> , 2013, 101, 221-228.	2.9	13
24	The genome sequence of the soft-rot fungus <i>Penicillium purpurogenum</i> reveals a high gene dosage for lignocellulolytic enzymes. <i>Mycology</i> , 2018, 9, 59-69.	4.4	12
25	Global gene expression analysis provides insight into local adaptation to geothermal streams in tadpoles of the Andean toad <i>Rhinella spinulosa</i> . <i>Scientific Reports</i> , 2017, 7, 1966.	3.3	10
26	Fast-SG: an alignment-free algorithm for hybrid assembly. <i>GigaScience</i> , 2018, 7, .	6.4	8
27	The relevance of enzyme specificity for coenzymes and the presence of 6-phosphogluconate dehydrogenase for polyhydroxyalkanoates production in the metabolism of <i>Pseudomonas</i> sp. LFM046. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 240-250.	7.5	8
28	<i>Mycoplasma hyopneumoniae</i> J elicits an antioxidant response and decreases the expression of ciliary genes in infected swine epithelial cells. <i>Scientific Reports</i> , 2020, 10, 13707.	3.3	6