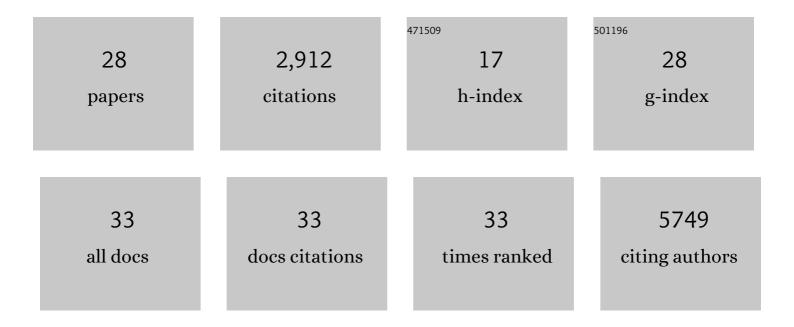
Alex Di Genova

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3889940/publications.pdf

Version: 2024-02-01



#	Article	IF	CITATIONS
1	The Atlantic salmon genome provides insights into rediploidization. Nature, 2016, 533, 200-205.	27.8	1,021
2	The BioMart community portal: an innovative alternative to large, centralized data repositories. Nucleic Acids Research, 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. G3: Genes, Genomes, Genetics, 2013, 3, 2031-2047.	1.8	244
4	Genome-wide association analysis reveals loci associated with resistance against Piscirickettsia salmonis in two Atlantic salmon (Salmo salar L.) chromosomes. BMC Genomics, 2015, 16, 854.	2.8	120
5	Whole genome comparison between table and wine grapes reveals a comprehensive catalog of structural variants. BMC Plant Biology, 2014, 14, 7.	3.6	115

6 Genome wide association study for resistance to Caligus rogercresseyi in Atlantic salmon (Salmo) Tj ETQq0 0 0 rgB3.5 Overlock 10 Tf 50

7	The bioleaching potential of a bacterial consortium. Bioresource Technology, 2016, 218, 659-666.	9.6	63
8	Genomic variation underlying complex life-history traits revealed by genome sequencing in Chinook salmon. Proceedings of the Royal Society B: Biological Sciences, 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. Evolutionary Applications, 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. BMC Genomics, 2013, 14, 878.	2.8	50
11	A new genome of Acidithiobacillus thiooxidans provides insights into adaptation to a bioleaching environment. Research in Microbiology, 2014, 165, 743-752.	2.1	48
12	Efficient hybrid de novo assembly of human genomes with WENGAN. Nature Biotechnology, 2021, 39, 422-430.	17.5	47
13	Reconstruction of the microalga Nannochloropsis salina genome-scale metabolic model with applications to lipid production. BMC Systems Biology, 2017, 11, 66.	3.0	41
14	The transposable element-rich genome of the cereal pest Sitophilus oryzae. BMC Biology, 2021, 19, 241.	3.8	40
15	Transcriptome sequencing of Prunus sp. rootstocks roots to identify candidate genes involved in the response to root hypoxia. Tree Genetics and Genomes, 2015, 11, 1.	1.6	34
16	SalmonDB: a bioinformatics resource for Salmo salar and Oncorhynchus mykiss. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar050-bar050.	3.0	28
17	Genome wide identification of Acidithiobacillus ferrooxidans (ATCC 23270) transcription factors and comparative analysis of ArsR and MerR metal regulators. BioMetals, 2012, 25, 75-93.	4.1	21
18	Transcriptome profiling of grapevine seedless segregants during berry development reveals candidate genes associated with berry weight. BMC Plant Biology, 2016, 16, 104.	3.6	18

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#	Article	IF	CITATIONS
19	Identification of SNPs and InDels associated with berry size in table grapes integrating genetic and transcriptomic approaches. BMC Plant Biology, 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. Biological Research, 2020, 53, 15.	3.4	18
21	Cdk5 regulates Rap1 activity. Neurochemistry International, 2013, 62, 848-853.	3.8	15
22	RNA-Seq analysis and transcriptome assembly of raspberry fruit (Rubus idaeus ¨Heritage¨) revealed several candidate genes involved in fruit development and ripening. Scientia Horticulturae, 2019, 254, 26-34.	3.6	15
23	Bioinformatic survey for new physiological substrates of Cyclin-dependent kinase 5. Genomics, 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. Mycology, 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 Rhinella spinulosa. Scientific Reports, 2017, 7, 1966.	3.3	10
26	Fast-SG: an alignment-free algorithm for hybrid assembly. GigaScience, 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 Pseudomonas sp. LFM046. International Journal of Biological Macromolecules, 2020, 163, 240-250.	7.5	8
28	Mycoplasma hyopneumoniae J elicits an antioxidant response and decreases the expression of ciliary genes in infected swine epithelial cells. Scientific Reports, 2020, 10, 13707.	3.3	6